

DE AA505075-derived oligonucleotide SEQ ID 4947.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; 88; primer.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Myce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI, 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4947; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX 1520 AAAAAAAAAAGTAAAA 1537

Db ||||| |||||
1 AAAAAAAAAAAAAAAAAA 18
RESULT 752
ABD25936
ID ABD25936 standard; DNA, 20 BP.
XX
XX ABD25936;
AC
XX 29-JUL-2004 (first entry)
DT
XX
XX AA505075-derived oligonucleotide SEQ ID 4948.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; 88; primer.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
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XX 23-APR-2002; 2002WO-US013143.
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XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
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XX Myce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
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XX WPI, 2003-093058/08.
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XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4948; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SO Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 753

ABD32081/C
ID ABD32081 standard; DNA; 20 BP.

XX AC ABD32081;

XX DT 29-JUL-2004 (first entry)

DE Human PDE4C-derived oligonucleotide SEQ ID 14292.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 14292; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SO Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 754

ABD21541/C
ID ABD21541 standard; DNA; 20 BP.

XX AC ABD21541;

XX DT 29-JUL-2004 (first entry)

DE S100 calcium binding protein A2-derived oligo SEQ ID 553.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 553; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, allergies and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.4e+02; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAA 1537

Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 755

ABD25671

ID ABD25671 standard; DNA; 20 BP.

XX ABD25671;

XX 29-JUL-2004 (first entry)

XX A1024215-derived oligonucleotide SEQ ID 4683.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPFIG-) EPIGENESIS PHARM INC.

XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahbuddin S;

XX WPI; 2003-093058/08.
XX
XX pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nuclear acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.

XX Claim 15; SEQ ID NO 4683; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
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XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
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XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, allergies and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.4e+02; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAA 1537

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 756

ABD21765

ID ABD21765 standard; DNA; 20 BP.

XX ABD21765;

XX 29-JUL-2004 (first entry)

XX Human stannocalcin-derived oligo SEQ ID 777.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

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PN WO200285309-A2.
XX
XX 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
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XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmacutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 777; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC polynary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 2 AAAAAAAAAAGTAAAA 19
RESULT 757
ABD24675
ID ABD24675 standard; DNA; 20 BP.
XX
XX ABD24675;
XX
XX 29-JUL-2004 (first entry)
XX
DE AA281534-derived oligonucleotide SEQ ID 3687.
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XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
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XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
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XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
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XX Pharmacutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 3687; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
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CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
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CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
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XX
XX Sequence 20 BP; 1 A; 3 C; 6 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 716 TTCTGTTTGTGCTGTG 733
|||||||
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Db 2 TTCTCTGTTCTGCTGTTG 19

RESULT 759

ABD26880 standard; DNA; 20 BP.

ABD26880;

29-JUL-2004 (first entry)

AA278764-derived oligonucleotide SEQ ID 5892.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

Homo sapiens.

MO200285309-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIC-) EPICGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S; WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 5892; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers; (b) the oligonucleotides; (c) instructions for adding a carrier and for use of the kit. The composition of the invention has anti-allergic, anti-inflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidine present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

SO Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 759

ABD24850 standard; DNA; 20 BP.

ABD24850;

29-JUL-2004 (first entry)

A1092623-derived oligonucleotide SEQ ID 3862.

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

Homo sapiens.

MO200285309-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIC-) EPICGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S; WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 3862; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers; (b) the oligonucleotides; (c) instructions for adding a carrier and for use of the kit. The composition of the invention has anti-allergic, anti-inflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered

DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
PS Claim 15; SEQ ID NO 3508; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
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CC surfactant depletion or hyposecretion, when administered to a mammal. The
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CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
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CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability of target polypeptide present in the lungs. The
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasocostriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAGTAA 1536
DB 3 TAAAAAAGTAA 20
RESULT 762
ABD25532
ID ABD25532 standard; DNA; 20 BP.
XX
XX ABD25532;
DT 29-JUN-2004 (first entry)
XX
DE A1125651-derived oligonucleotide SEQ ID 4544.
XX
XX Human, antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasocostriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX
XX W0200285309-A2.

XX
PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPICGENESIS PHARM INC.
XX
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
PS Claim 15; SEQ ID NO 4544; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
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CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
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CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
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CC inflammation, allergies and/or surfactant hypoproduction are associated
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CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAGTAA 1537
DB 1 AAAAAAAGTAA 18
RESULT 763
ABD25046
ID ABD25046 standard; DNA; 20 BP.
XX
XX ABD25046;
DT 29-JUN-2004 (first entry)
XX
DE A1128305-derived oligonucleotide SEQ ID 4058.
XX

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
respiratory tract inflammation; adenosine sensitivity; lung; cancer;
surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN W0200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002MO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyece JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
DR WPI; 2003-093058/08.
XX
PF Pharmaceutical composition for treating asthma, has antisense
PF oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4058; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
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CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTMAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 764
ABD29094
ID ABD29094 standard; DNA: 20 BP.
XX
AC ABD29094;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA679352-derived oligonucleotide SEQ ID 8106.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN W0200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002MO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyece JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
DR WPI; 2003-093058/08.
XX
PF Pharmaceutical composition for treating asthma, has antisense
PF oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 8106; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 12 A; 1 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1512 TGTTCATTAAAAAAA 1529
Dd 3 TGTCAAGTAAAAAAA 20
RESULT 765
ABD21825
ID ABD21825 standard; DNA; 20 BP.
XX
AC ABD21825;
XX
DT 29-JUL-2004 (first entry)
DE Human stannocalcin-derived oligo SEQ ID 837.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiaesthetic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
PI Nyce JM, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
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XX WPI, 2003-093058/08.
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XX
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CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
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CC or availability, or to increase the degradation of the target mRNA or to
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CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
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XX
SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 723 TTTTGCTGTGCTGCTGC 740
Dd 1 TTGTGCTGCTGCTGCTGC 18
RESULT 766
ABD23911/C
ID ABD23911 standard; DNA; 20 BP.
XX
AC ABD23911;
XX
DT 29-JUL-2004 (first entry)
DE Human calmodulin 2-derived oligonucleotide SEQ ID 2923.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiaesthetic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
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PA (EPIC-) EPIGENESIS PHARM INC.
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XX WPI, 2003-093058/08.
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XX
PS Claim 15; SEQ ID NO 2923; 763pp; English.
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XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity. Levels of adenosine (A) or (A) receptors,

Query	Match	Score	DB	Length
1520	AAAAAAAAAACTAAAA	1537		
19	AAAAAAAAAAAAAAAAA	2		
Result 767				
ABD25044	ID	ABD25044	standard; DNA; 20 BP.	
ABD25044				
29-JUL-2004	(first entry)			
A1128305-derived oligonucleotide SEQ ID 4056.				
Human; antiense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant production; anti-allergic; anti-inflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.				
Homo sapiens.				
WO200285309-A2.				
31-OCT-2002.				
23-APR-2002; 2002WO-US013143.				
24-APR-2001; 2001US-0286036P.				
(EPIC-) EPIGENESIS PHARM INC.				
Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D, Miller S, Tang L, Shahabuddin S,				
WPI; 2003-093058/08.				

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XX
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CC comprising oligonucleotides, effective for alleviating
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CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
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CC transplantation rejection, pulmonary infections, bronchitis or cancer.
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CC prevent any unwanted effects due to it

XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX
XX
XX Query March 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4,4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
|||||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 768
ID2 ABD25111
XX ABD25111 standard; DNA; 20 BP.
XX
XX ABD25111;
XX
XX 29-JUL-2004 (first entry)
XX
XX A1125228-derived oligonucleotide SEQ ID 4123.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.

XX
XX Homo sapiens.
XX
XX W0200285309-A2.

PD 31-OCT-2002.
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PF 23-APR-2002; 2002WO-US013143.
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PR 24-APR-2001; 2001US-0286036P.
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PA (EPIC-) EPIGENESIS PHARM INC.
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DR WPI; 2003-093058/08.
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PT Pharmaceutical composition for treating asthma, has antilease
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PS Claim 15; SEQ ID NO 4123; 763pp; English.
XX
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CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
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CC with a disease or condition such as pulmonary vasooconstriction,
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CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidine present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 769
ADH08684
ID ADH08684 standard; DNA; 20 BP.
XX
AC ADH08684;
XX
DT 11-MAR-2004 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KM Linking oligonucleotide; ss; nucleic acid detection;

KM nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PM US2002137070-A1.
XX
PD 26-SEP-2002.
XX
PF 10-OCT-2001; 2001US-00973638.
XX
XX 29-JUL-1996; 96US-001809P.
XX 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mickin CA, Letsinger RL, Mucic RC, Stornhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2004-059018/06.
XX
XX Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
PS Example 18; SEQ ID NO 55; 130pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 770
ADH08814
ID ADH08814 standard; DNA; 20 BP.
XX
AC ADH08814;
XX
DT 11-MAR-2004 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KM Linking oligonucleotide; ss; nucleic acid detection;
KM nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PM US2002137072-A1.
XX
PD 26-SEP-2002.
XX
PF 12-OCT-2001; 2001US-00976617.

```
XX 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
PA
PI Murkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
PI Taton TA;
XX
XX WPI; 2004-059020/06.
XX
XX Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
XX Example 18; SEQ ID NO 55; 130pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 86.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 771
XX ADH08749
XX ID ADH08749 standard; DNA; 20 BP.
XX AC ADH08749;
XX
XX 11-MAR-2004 (first entry)
XX
XX Nanotechnology nucleic acid detection method associated #54.
DE
XX Linking oligonucleotide; ss; nucleic acid detection;
XX nanoparticle-oligonucleotide conjugate.
XX
XX Synthetic.
XX
XX US2002137071-A1.
XX
XX 26-SEP-2002.
XX
XX 10-OCT-2001; 2001US-00974007.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
PA
```

```
XX Murkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
PI Taton TA;
XX
XX WPI; 2004-059019/06.
XX
XX Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
XX Example 18; SEQ ID NO 55; 130pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 772
XX ADH65941/C
XX ID ADH65941 standard; DNA; 20 BP.
XX AC ADH65941;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human glucocorticoid receptor-specific antisense oligonucleotide #2775.
DE
XX antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX Homo sapiens.
XX
XX WO2003099215-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016084.
XX
XX 20-MAY-2002; 2002US-0381857P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Crosby SD, Nalseth AE;
XX
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 2775; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
CC
```

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CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, the
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 3 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1522 AAAAAAAAAAGTAAAG 1539
|||||
19 AAGAGAAAAATTAAGG 2
RESULT 773
ADH67409/C
ID ADH67409 standard; DNA; 20 BP.
XX
AC ADH67409;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4243.
XX
KM Antisense oligonucleotide; glucocorticoid receptor; infection;
KM inflammation; tumour formation; diabetes; obesity;
KM cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KM phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4243; 985bp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, the
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1521 AAAAAAAAAAGTAAAG 1538
|||||
Db 20 AAAAAAAAAAAAAAAAAAG 3
|||||
RESULT 774
AD134492
ID AD134492 standard; DNA; 20 BP.
XX
AC AD134492;
XX
DT 22-APR-2004 (first entry)
XX
DE Nucleotide sequence of a dA20 oligonucleotide.
XX
KM Nucleic acid amplification; RNA transcription; RNA polymerase; ss; T7.
XX
OS Synthetic.
XX
PN WO2003102243-A1.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-US017103.
XX
PR 31-MAY-2002; 2002US-0384454P.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Kamme FC, Zhu JY;
XX
DR WPI; 2004-035466/03.
XX
PT Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating
PT single-stranded oligonucleotide from the transcription sample.
XX
PS Example 2; SEQ ID NO 11; 26pp; English.
XX
CC The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction. The
CC present sequence represents an oligonucleotide used to exemplify RNA
CC transcription in the presence of single- and double-stranded
CC oligonucleotides.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAG 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAAA 18
|||||
RESULT 775
AD147212
ID AD147212 standard; DNA; 20 BP.
XX
AC AD147212;
XX
DT 22-APR-2004 (first entry)
```

XX DE Molecule analysing microchannel method related probe #2.
XX KM laminar flow; micro channel; complex; selectively promoted; fluorescence;
XX KW probe; ss.
XX OS Unidentified.
XX XX WO2004010140-A1.
XX PN 29-JAN-2004.
XX PD 18-JUL-2003; 2003WO-JP009142.
XX PE 19-JUL-2002; 2002JP-00211462.
XX PR 19-JUL-2002; 2002JP-00211462.
XX XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PA Yamashita K, Maeda H, Shimizu H, Miyazaki M, Nakamura H,
XX PI Yamaguchi Y;
XX XX WPI; 2004-180318/17.
XX DR
XX PT Analysis of sample molecules such as DNA fragment, by using micro channel
XX PT to form laminar flow of specimen molecule-containing solution and complex
XX PT forming molecule containing solution.
XX PS Example 1; Page 9; 19pp; Japanese.
XX CC The invention relates to a novel method involving forming a laminar flow,
XX CC by passing into a micro channel, a solution containing the specimen
XX CC molecules, and a solution containing probe molecules capable of forming a
XX CC complex with the specimen molecules. The dispersion of the formed complex
XX CC is selectively promoted, based on their affinity, and the degree of
XX CC dispersion of the complex formed between the specimen molecules and the
XX CC probe molecules is detected and analysed. The probe molecules are capable
XX CC of producing fluorescence. This polynucleotide sequence represents an
XX CC oligo used in the exemplification of the invention.
XX SO Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAAA 1537
XX DB 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 776
XX ADJ51142/c
XX ID ADJ51142 standard; DNA; 20 BP.
XX XX
XX AC ADJ51142;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE Polyalkyleneamine-conjugated oligonucleotide #1.
XX XX ss; Antimicrobial; Antiinflammatory; Cytostatic; prodrug; infection;
XX KM inflammation; tumour.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 20
XX FT /+tag= a
XX FT /mod_base= OTHER
XX FT /note= "Optionally conjugated with spermine,
XX FT polyethylentimine (PEI) 600 or PEI 1200,
XX FT tetraethylenpentamine. Also optionally 5'-protected with
XX FT DMT."

XX XX US2004019000-A1.
XX PN 23-JAN-2004.
XX PD 19-JUL-2002; 2002US-00199585.
XX XX
XX PE 19-JUL-2002; 2002US-00199585.
XX PR 19-JUL-2002; 2002US-00199585.
XX XX
XX XX (MANO/) MANOHARAN M.
XX PA (GUZA/) GUZAEV A P.
XX PA (MAIE/) MAIER M A.
XX XX
XX PT Manoharan M, Guzaev AP, Maier MA,
XX XX WPI; 2004-224429/21.
XX DR
XX XX
XX PT Novel polyalkyleneamine-containing oligomeric compound useful for
XX PT preventing or delaying infection, inflammation or tumor formation in
XX PT organisms.
XX PS Example 3; Page 22; 37pp; English.
XX XX
XX CC The invention relates to a polyalkyleneamine-containing oligomeric
XX CC compound (OC). Also described is a compound (C) comprising an oligomeric
XX CC part, a fusogenic part, and a targeting part; and enhancing the cellular
XX CC uptake of OC, by conjugating OC to a fusogenic part. In (C), the
XX CC fusogenic part is covalently linked to the oligomeric part. The targeting
XX CC part is covalently linked to the oligomeric or fusogenic part, where the
XX CC fusogenic part is a lipophilic polyamine, polyethylentimine,
XX CC polyallylamine, fusogenic peptide, oligomeric imidazole, histidine,
XX CC pyridine, hydroxylamine, substituted hydroxylamine, hydrazine,
XX CC substituted hydrazine, thiourea or imine. The targeting part is a ligand
XX CC that binds to a cellular reporter, where the targeting part is
XX CC transferrin, folate, epidermal growth factor, nerve growth factor,
XX CC insulin, alpha-fetoprotein, galactose, galactosamine, lactose, mannose, a
XX CC polyclonal antibody, monoclonal antibody, vitamin B12, ibuprofen,
XX CC cholesterol, low-density lipoprotein, peptide comprising an arginine-
XX CC glycine-aspartic acid sequence. The oligomeric part is an
XX CC oligonucleotide, and oligonucleotide analogue, a peptide nucleic acid or
XX CC a peptide nucleic acid analogue. OC is useful as a prodrug, useful in
XX CC diagnostics, therapeutics and as research reagents and kits. OC is useful
XX CC for preventing or delaying infection, inflammation or tumour formation in
XX CC organisms. The present sequence represents an oligonucleotide used in the
XX CC method of the invention.
XX SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAAA 1537
XX DB 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 777
XX ADK98410/c
XX ID ADK98410 standard; DNA; 20 BP.
XX XX
XX AC ADK98410;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE Primer of the invention #4130.
XX XX
XX KM human; single nucleotide polymorphism; SNP; ss; primer.
XX OS Synthetic.
XX XX
XX PN JP2003259875-A.
XX XX


```
PD 16-SEP-2003.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-093977/10.
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
XX fragment from another set of sequences, or for detecting single
XX nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 7439; 2627bp; Japanese.
XX
XX The present invention relates to a polynucleotide isolated from a human
XX gene and is useful for detecting a single nucleotide polymorphism in a
XX human gene or for diagnosing of disease. The invention enables the
XX detection of a single nucleotide polymorphism in a human gene. The
XX present sequence represents a primer of the invention.
XX
XX Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 668 CTCACCTCTGACGCCGCT 665
Db 19 CTCACCTCTGAGCCTCT 2
RESULT 778
ADJ60935/C
ID ADJ60935 standard; DNA; 20 BP.
XX
XX ADJ60935;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Oligonucleotide associated to PDE4C #1.
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
XX Homo sapiens.
XX
XX WO2004011613-A2.
XX
XX 05-FEB-2004.
PD
XX
XX 25-JUL-2003; 2003WO-US023509.
XX
XX 29-JUL-2002; 2002US-0399076P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Tang L, Sandraegra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.,
XX initiation codons and introns of respiratory disease-relevant genes e.g.,
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX disease e.g., asthma.
XX
XX Claim 2; SEQ ID NO 1791; 85bp; English.
XX
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CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAACTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 779
ADJ32920
ID ADJ32920 standard; DNA; 20 BP.
XX
XX ADJ32920;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Oligo related to thiol oligo-gold colloid conjugate probe SEQ 70.
XX
XX nanoparticle; gold; disease; forensic; paternity testing.
XX cell line authentication; gene therapy; ss; gold colloid conjugate.
XX
XX Synthetic.
XX
XX US2003207296-A1.
XX
XX 06-NOV-2003.
XX
XX 08-OCT-2002; 2002US-00266983.
XX
XX 29-JUL-1996; 96US-0031809P.
XX
XX 21-JUL-1997; 97WO-US012783.
XX
XX 29-JAN-1999; 99US-00240755.
XX
XX 25-JUN-1999; 99US-00344667.
XX
XX 13-JAN-2000; 2000US-0176409P.
XX
XX 28-MAR-2000; 2000US-0192699P.
XX
XX 26-APR-2000; 2000US-0200161P.
XX
XX 26-JUN-2000; 2000US-00603830.
XX
XX 26-JUN-2000; 2000US-0213906P.
XX
XX 11-AUG-2000; 2000US-0224631P.
XX
XX 08-DEC-2000; 2000US-0254392P.
XX
XX 08-DEC-2000; 2000US-0254418P.
XX
XX 11-DEC-2000; 2000US-0255235P.
XX
XX 11-DEC-2000; 2000US-0255236P.
XX
XX 12-JAN-2001; 2001US-00760500.
XX
XX 28-MAR-2001; 2001US-00820279.
XX
XX 09-APR-2001; 2001US-0282640P.
XX
XX 10-AUG-2001; 2001US-00927777.
XX
XX 09-OCT-2001; 2001US-0327864P.
XX
XX 07-DEC-2001; 2001US-00008978.
XX
XX (PARK/) PARK S.
XX (TATO/) TATON T A.
XX (MIRK/) MIRKIN C A.
```

```
XX Park S, Taton TA, Mirkin CA;
XX WPI; 2004-059754/06.
PT Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting
PT nucleic acid with different types of nanoparticles having attached
PT oligonucleotides and observing detectable change brought about by
PT hybridization.
XX
PS Example 24; SEQ ID NO 70; 206bp; English.
XX
CC The invention relates to a novel method for detecting a nucleic acid
CC having at least two portions comprising contacting the nucleic acid with
CC at least two types of nanoparticles, such as gold, having attached
CC oligonucleotides and observing a detectable change brought about by
CC hybridisation of the oligonucleotides on the nanoparticles with the
CC nucleic acid. The method of the invention may be useful for detecting a
CC nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene
CC associated with a disease, a fungal DNA, synthetic DNA or RNA,
CC structurally modified natural or synthetic DNA or RNA or a product of a
CC polymerase chain reaction amplification. The detected nucleic acid may be
CC utilised for diagnosis of disease, sequencing of nucleic acids,
CC forensics, paternity testing, cell line authentication and monitoring
CC gene therapy. The method for detecting the nucleic acids is based on
CC observing a colour change with the naked eye and is cheap, fast, simple,
CC and robust, requiring no specialised or expensive equipment. The current
CC sequence is that of the oligonucleotide which is related to a thiol-
CC modified oligonucleotide-gold colloid conjugate probe of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 780
AD132905
ID AD132905 standard; DNA; 20 BP.
XX
AC AD132905;
XX
XX 06-MAY-2004 (first entry)
XX
DE Synthetic thiol-modified oligo-gold colloid conjugate probe - SEQ 55.
XX
KM nanoparticle; gold; disease; forensic; paternity testing;
KM cell line authentication; gene therapy; ss; gold colloid conjugate;
KM probe.
XX
OS Synthetic.
XX
XX US2003207296-A1.
XX
XX 06-NOV-2003.
XX
XX 08-OCT-2002; 2002US-00266983.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97MO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 13-JAN-2000; 2000US-0176409P.
XX 28-MAR-2000; 2000US-0192699P.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX 26-JUN-2000; 2000US-0213906P.
XX 11-AUG-2000; 2000US-0224631P.
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PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
XX
XX (PARK/) PARK S.
XX (TATON/) TATON T A.
XX (MIRK/) MIRKIN C A.
XX
PI Park S, Taton TA, Mirkin CA;
XX WPI; 2004-059754/06.
XX
DR WPI; 2004-059754/06.
XX
XX Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting
XX nucleic acid with different types of nanoparticles having attached
XX oligonucleotides and observing detectable change brought about by
XX hybridization.
XX
PS Example 18; SEQ ID NO 55; 206bp; English.
XX
XX The invention relates to a novel method for detecting a nucleic acid
XX having at least two portions comprising contacting the nucleic acid with
XX at least two types of nanoparticles, such as gold, having attached
XX oligonucleotides and observing a detectable change brought about by
XX hybridisation of the oligonucleotides on the nanoparticles with the
XX nucleic acid. The method of the invention may be useful for detecting a
XX nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene
XX associated with a disease, a fungal DNA, synthetic DNA or RNA,
XX structurally modified natural or synthetic DNA or RNA or a product of a
XX polymerase chain reaction amplification. The detected nucleic acid may be
XX utilised for diagnosis of disease, sequencing of nucleic acids,
XX forensics, paternity testing, cell line authentication and monitoring
XX gene therapy. The method for detecting the nucleic acids is based on
XX observing a colour change with the naked eye and is cheap, fast, simple,
XX and robust, requiring no specialised or expensive equipment. The current
XX sequence is that of the synthetic thiol-modified oligonucleotide-gold
XX colloid conjugate probe of the invention which is linked via a thiol
XX group to a gold nanoparticle.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 781
ADK70840
ID ADK70840 standard; DNA; 20 BP.
XX
XX ADK70840;
XX
XX 06-MAY-2004 (first entry)
XX
DE 5' mRNA DNA preparation method related tag DNA sequence #8.
XX
XX DNA preparation; 5' mRNA; linker synthesis; primer synthesis;
XX gene regulation; gene expression; ss; tag.
XX
OS Unidentified.
XX
XX W02003106672-A2.
XX
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PD 24-DEC-2003.
XX
XX 12-JUN-2003; 2003WO-JP007514.
XX
XX 12-JUN-2002; 2002JP-00171851.
XX
XX 12-AUG-2002; 2002JP-00235294.
XX
XX (RIKE ) RIKEN KK.
XX (DNAF-) DNAFORM KK.
XX
XX Hayashizaki Y, Carninci P, Harbers MT;
XX
XX WPI; 2004-082194/08.
XX
XX Preparing DNA fragment corresponding to nucleotide sequence of 5' end
XX region of mRNA, by preparing nucleic acid corresponding to nucleotide
XX sequence of 5' end of mRNA, cleaving nucleic acid with restriction
XX enzyme.
XX
XX Example 5; SEQ ID NO 40; 121bp; English.
XX
XX The invention comprises a method for preparing a DNA fragment
XX corresponding to a nucleotide sequence of a 5' end of an mRNA. The method
XX is useful for synthesizing a nucleotide sequence to be used as a linker
XX or primer and selectively collecting multiple nucleic acid fragments
XX containing information on the nucleotide sequences at the 5' end of
XX multiple mRNA in a sample. The method is also useful for identifying
XX regions in the genome, which are required for gene regulation and gene
XX expression. The present DNA sequence was used in an example of the
XX invention.
XX
XX Sequence 20 BP; 0 A; 1 C; 10 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 545 TGTGCGTGGCGTGGCGTG 562
XX |||||
XX 2 TGTGTGTGTGTGTGCGTG 19
XX
XX RESULT 782
XX ADK69880/C
XX ID ADK69880 standard; DNA; 20 BP.
XX
XX AC ADK69880;
XX
XX 06-MAY-2004 (first entry)
XX
XX Sulphurised oligonucleotide #10.
XX
XX Phosphorothioate backbone; sulphurised oligonucleotide; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; 2'-O-methoxyethyl
XX residues"
XX
XX US2003212267-A1.
XX
XX 13-NOV-2003.
XX
XX 12-DEC-2002; 2002US-00181200.
XX
XX 11-JAN-2000; 2000US-00481486.
XX
XX 10-JAN-2001; 2001WO-US000715.
XX
XX (COLE/) COLE D L.
XX

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PA (RAVI/) RAVIKUMAR V T.
XX (CHER/) CHERUVALLATH Z S.
XX
XX Cole DL, Ravikumar VT, Chervuallath ZS;
XX
XX WPI; 2004-069376/07.
XX
XX Preparation of phosphorothioate oligonucleotides involves oxidizing
XX phosphite intermediate with acetyl disulfide in acetonitrile for time to
XX effect conversion of phosphite intermediate to phosphorothioate.
XX
XX Example 12; SEQ ID NO 10; 8bp; English.
XX
XX The invention relates to phosphorothioate oligonucleotides having
XX nucleoside with 240 modification are prepared by phosphorylating 5'-
XX hydroxyl of a nucleic acid moiety having a nucleoside with 2'
XX modification in an acetonitrile containing solvent mixture to form a
XX phosphite intermediate; and oxidizing the phosphite intermediate with an
XX acetyl disulfide in an acetonitrile for a time to effect conversion of
XX the phosphite intermediate to phosphorothioate. The invented method
XX achieves high yields and greater efficiency. The present sequence is
XX sulphurised oligonucleotide used in the exemplification of the invention.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX |||||
XX 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 783
XX ADK69885/C
XX ID ADK69885 standard; DNA; 20 BP.
XX
XX AC ADK69885;
XX
XX 06-MAY-2004 (first entry)
XX
XX Sulphurised oligonucleotide #15.
XX
XX Phosphorothioate backbone; sulphurised oligonucleotide; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; 2'-O-methoxyethyl
XX residues"
XX
XX US2003212267-A1.
XX
XX 13-NOV-2003.
XX
XX 12-DEC-2002; 2002US-00181200.
XX
XX 11-JAN-2000; 2000US-00481486.
XX
XX 10-JAN-2001; 2001WO-US000715.
XX
XX (COLE/) COLE D L.
XX (RAVI/) RAVIKUMAR V T.
XX (CHER/) CHERUVALLATH Z S.
XX
XX Cole DL, Ravikumar VT, Chervuallath ZS;
XX
XX WPI; 2004-069376/07.
XX
XX Preparation of phosphorothioate oligonucleotides involves oxidizing
XX

```

PT phosphite intermediate with acetyl disulfide in acetonitrile for time to
PT effect conversion of phosphite intermediate to phosphorothioate.
XX
PS Example 22; SEQ ID NO 15; 8bp; English.
XX
CC The invention relates to phosphorothioate oligonucleotides having
CC nucleoside with 240 modification are prepared by phosphorylating 5'-
CC hydroxyl of a nucleic acid moiety having a nucleoside with 2'
CC modification in an acetonitrile containing solvent mixture to form a
CC phosphite intermediate; and oxidizing the phosphite intermediate with an
CC acetyl disulfide in an acetonitrile for a time to effect conversion of
CC the phosphite intermediate to phosphorothioate. The present method
CC achieves high yields and greater efficiency. The present sequence is
CC sulphurised oligonucleotide used in the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 784
ADK74647/c
ID ADK74647 standard; DNA; 20 BP.
XX
AC ADK74647;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.
XX
KM Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1981; 417bp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy, or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 785
ADK74188/c
ID ADK74188 standard; DNA; 20 BP.
XX
AC ADK74188;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1522.
XX
KM Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1522; 417bp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy, or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2
RESULT 786
ADK74969/C
ID ADK74969 standard; DNA; 20 BP.
AC ADK74969;
XX
XX ADK74969;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2303.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 2303; 417pp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'OH wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 787
ADK75847
ID ADK75847 standard; DNA; 20 BP.
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AC ADK75847;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #3181.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 3181; 417pp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'OH wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 7 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1165 AGTATTGTTGAATAGT 1182
DB 3 AGTATTGTTAAACAGT 20
RESULT 788
ADK79524/C
ID ADK79524 standard; DNA; 20 BP.
AC ADK79524;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #6858.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
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OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 6858; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 11 A; 1 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1252 TTTTGTTTTTAAATCAGA 1269
XX ||||| ||||| |||||
XX TTTTGATTTTAAATCACA 3
XX
XX RESULT 789
XX ADK74688/C
XX ID ADK74688 standard; DNA; 20 BP.
XX
XX ADK74688;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2022.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
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PA (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 2022; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX ||||| ||||| |||||
XX AAAAAAAAAAAGTAAAA 1
XX
XX RESULT 790
XX ADK74889/C
XX ID ADK74889 standard; DNA; 20 BP.
XX
XX ADK74889;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2223.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
```


XX Claim 4, SEQ ID NO 2223; 417bp; English.
PS
XX The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a decoy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAATAAAA 1537
Db ||||||||| |||||
20 AAAAAAAAAAAAAAAAAA 3

RESULT 791
ADK80788/C
ID ADK80788 standard; DNA; 20 BP.
AC
XX ADK80788;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8122.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4, SEQ ID NO 8122; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a decoy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 10 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1252 TTTGTTTAAATCAGA 1269
Db ||||||||| |||||
18 TTTGATTTTAAATCACA 1

RESULT 792
ADK74838/C
ID ADK74838 standard; DNA; 20 BP.
AC
XX ADK74838;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2172.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4, SEQ ID NO 2172; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1521 AAAAAAAAAAGTAAAG 1538
DB 20 AAAAAAAAAAAAAAAAAAG 3

RESULT 793
ADK77218
ID ADK77218 standard; DNA; 20 BP.
XX
XX ADK77218;
XX AC
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #4552.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX MO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003MO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 4552; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1165 AGTATTGTTGAAATAGT 1182
DB 2 AGTATTGTTAAACAGT 19

RESULT 794

ADK80450/C
ID ADK80450 standard; DNA; 20 BP.
XX
XX ADK80450;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #7784.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX MO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003MO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX

PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 7784; 417bp; English.

XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a decoy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX

XX
XX Sequence 20 BP; 10 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1252 TTTTGTGTTTAAATCAGA 1269
XX
XX 19 TTTTGTGTTTAAATCACA 2

RESULT 795

ADM69507

ID

ADM69507 standard; DNA; 20 BP.

XX

XX ADM69507;

XX

XX 03-JUN-2004 (first entry)

XX

XX Plant gene polymorphism marker related primer, SEQ ID 386.

XX Primer; variation mapping; mutation mapping; plant;

KM gene polymorphism marker; ss.
XX Synthetic.
OS
XX JP2003289885-A.
XX
XX 14-OCT-2003.
XX
XX 31-JAN-2003; 2003JP-00024620.
XX
XX 01-FEB-2002; 2002JP-00025338.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (SAIM-) SAI MEDIA KK.
XX (MATS/) MATSUI M.
XX (NAKA/) NAKAZAWA M.
XX
XX WPI; 2004-126231/13.
XX
XX A primer set and method useful for mapping at least the
PT variation/mutation part of a plant gene using a gene polymorphism marker.
PS
XX Claim 7; SEQ ID NO 386; 120bp; Japanese.
XX
XX The present invention relates to a primer set and method for mapping at
CC least the variation/mutation part of the plant gene using a gene
CC polymorphism marker. A mutation site of the plant gene is mapped by
CC utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC prepared from a plant homozygously having a mutation to be an object of
CC the mapping; (b) A forward primer 1 containing a base corresponding to
CC the gene polymorphic marker of one ecotype plant, a forward primer 2
CC containing a base corresponding to the genetic polymorphism of the other
CC ecotype plant and a reverse primer 3 based on the base sequence common
CC with both the ecotype plants are prepared; (c) two kinds of
CC oligonucleotides emitting fluorescence of different colors when the
CC genetic polymorphism marker is detected are prepared; (d) an
CC amplification reaction of the genomic DNA is carried out in the presence
CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC the fluorescence intensity emitted from the resultant reactional product
CC is detected and (f) the position on the genome of the mutation site is
CC determined from the results of detection. The present sequence is a
XX primer, used to illustrate the invention.
XX
XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1462 AGAAGGTGACCAATTCA 1479
DB 1 AGAAGGTGACCACTTCA 18
RESULT 796
ADM69506
ID ADM69506 standard; DNA; 20 BP.
XX
XX ADM69506;
XX
XX 03-JUN-2004 (first entry)
XX
XX Plant gene polymorphism marker related primer, SEQ ID 385.
XX
XX primer; variation mapping; mutation mapping; plant;
KM gene polymorphism marker; ss.
XX Synthetic.
OS
XX JP2003289885-A.
XX
XX 14-OCT-2003.
XX
XX

PF 31-JAN-2003; 2003JP-00024620.
XX
XX 01-FEB-2002; 2002JP-00025338.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (SAIM-) SAI MEDIA KK.
XX (MATS/) MATSUI M.
XX (NAKA/) NAKAZAWA M.
XX
XX WPI; 2004-126231/13.
XX
XX A primer set and method useful for mapping at least the
PT variation/mutation part of a plant gene using a gene polymorphism marker.
PS
XX Claim 7; SEQ ID NO 385; 120bp; Japanese.
XX
XX The present invention relates to a primer set and method for mapping at
CC least the variation/mutation part of a plant gene using a gene
CC polymorphism marker. A mutation site of the plant gene is mapped by
CC utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC prepared from a plant homozygously having a mutation to be an object of
CC the mapping; (b) A forward primer 1 containing a base corresponding to
CC the gene polymorphic marker of one ecotype plant, a forward primer 2
CC containing a base corresponding to the genetic polymorphism of the other
CC ecotype plant and a reverse primer 3 based on the base sequence common
CC with both the ecotype plants are prepared; (c) two kinds of
CC oligonucleotides emitting fluorescence of different colors when the
CC genetic polymorphism marker is detected are prepared; (d) an
CC amplification reaction of the genomic DNA is carried out in the presence
CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC the fluorescence intensity emitted from the resultant reactional product
CC is detected and (f) the position on the genome of the mutation site is
CC determined from the results of detection. The present sequence is a
XX primer, used to illustrate the invention.
XX
XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1462 AGAAGGTGACCAATTCA 1479
DB 1 AGAAGGTGACCACTTCA 18
RESULT 797
ADL33726/C
ID ADL33726 standard; DNA; 20 BP.
XX
XX ADL33726;
XX
XX 03-JUN-2004 (first entry)
XX
XX LNA oligomer #5.
XX
XX Detection; isolation; locked nucleic acid; LNA; ss.
XX Synthetic.
OS
XX Key location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Optionally LNA nucleotides"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Optionally biotinylated or 5' A02-HEG3, where A0
FT is anthraquinone and HEG is hexa-ethylene glycol"
XX
XX W02004020575-A2.
XX
XX

XX	11-MAR-2004.
PD	
PF	20-JUN-2003; 2003WO-IB006354.
PR	24-JUN-2002; 2002US-0390928P.
PX	(EXIQ-) EXIQON AS.
PA	Kauppinen S, Jacobsen N;
XX	WP1; 2004-315512/29.
DR	
XX	Detecting and/or isolating nucleic acid molecule having homopolymeric
PT	sequence or repetitive element or conserved nucleotide sequence involves
FT	treating sample containing nucleic acid compounds with locked nucleic
PT	acid oligonucleotide.
XX	
XX	Claim 22; Page 51; 104pp; English.
PS	
XX	The present invention relates to a method (M1) for detecting and/or
CC	isolating a nucleic acid having a homopolymeric sequence or repetitive
CC	element or conserved nucleotide sequence. (M1) comprises treating a
CC	sample containing nucleic acid compounds with an locked nucleic acid
CC	(LNA) oligonucleotide (LO) to thereby detect and/or isolate a nucleic
CC	acid having the homopolymeric sequence or repetitive element or conserved
CC	nucleotide sequence. (M1) is useful for detecting and isolating nucleic
CC	acids released from a lysed complex biological mixture comprising nucleic
CC	acids. The present sequence is a LNA oligomer, used to illustrate the
CC	invention.
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1520 AAAAAAAAAAAGTAAA 1537 20 AAAAAAAAAAAAAAA 3
Db	
RESULT 798	
ID	ADLS9686 standard; DNA; 20 BP.
XX	
AC	ADLS9686;
XX	
DT	03-JUN-2004 (first entry)
DE	
XX	Human ESM-1 antisense oligonucleotide seqid 1935.
XX	
KW	cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW	gene therapy; endothelial specific molecule-1; ESM-1;
KW	ESM-1 related disorder; diabetes; cancer; ischemia; reperfusion injury;
KW	angiogenic disorder; immunological disorder; cardiovascular disorder;
XX	neurological disorder; antisense technology; ss.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorochioate backbone. All cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT	16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT	

[illegible]

```
FT modified_base 16.20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2004021978-A2.
XX
XX 18-MAR-2004.
XX
XX 19-AUG-2003; 2003WO-US025833.
XX
XX 19-AUG-2002; 2002US-040495P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX
XX Claim 3; SEQ ID NO 1952; 555bp; English.
XX
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).
XX
XX Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX 2 AAAAAAAAAAGCACAA 19
XX
XX RESULT 800
XX ADL59724
XX ID ADL59724 standard; DNA; 20 BP.
XX
XX AC ADL59724;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX Human ESM-1 antisense oligonucleotide seqid 1973.
XX
XX cytosolic; antidiabetic; immunomodulator; cardiant; neuroprotective;
XX gene therapy; endothelial specific molecule-1; ESM-1;
XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
XX angiogenic disorder; immunological disorder; cardiovascular disorder;
XX neurological disorder; antisense technology; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone. All cytidine
XX residues are 5-methylcytidines"
```

```
FT modified_base 1.5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX modified_base 16.20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2004021978-A2.
XX
XX 18-MAR-2004.
XX
XX 19-AUG-2003; 2003WO-US025833.
XX
XX 19-AUG-2002; 2002US-040495P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX
XX Claim 3; SEQ ID NO 1973; 555bp; English.
XX
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).
XX
XX Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX 3 AAAAAAAAAAGCACAA 20
XX
XX RESULT 801
XX ADM93653/C
XX ID ADM93653 standard; DNA; 20 BP.
XX
XX AC ADM93653;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX Human NOVX PCR primer #2.
XX
XX Human, NOVX; PCR; ss; congenital heart defect; cardiomyopathy;
XX atherosclerosis; hypertension; pulmonary stenosis; scleroderma;
XX adenocarcinoma; haemophilia; graft-versus-host disease; cancer;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX multiple sclerosis; diabetes; obesity; bronchial asthma;
XX acquired immunodeficiency syndrome; AIDS; Crohn's disease;
XX infectious disease; anorexia; immune disorder; primer.
XX
XX Homo sapiens.
XX
```


KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= C
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-043549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 179; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e-02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAA 1537
XX |||||||||
XX 20 AAAAAAAAAAAAAAAAAA 3

ADMI3994/C
ID ADMI3994 standard; DNA; 20 BP.
XX
XX A/C
XX ADMI3994;
XX
XX 01-JUN-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:181.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
OS
OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX 16..20
XX /tag= C
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX 16..20
XX /tag= C
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-043549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 181; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or

CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia and reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 804
ADM13999/C
ID ADM13999 standard; DNA, 20 BP.
XX
AC ADM13999;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:186.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritis; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*tag= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK,
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ichemia.
PS Claim 4; SEQ ID NO 186; 132pp; English.

XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compound,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridise with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. MPGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritis, vasotropic,
CC ophthalmological, immunomodulatory, and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 805
ADM14008/C
ID ADM14008 standard; DNA, 20 BP.
XX
AC ADM14008;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:195.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritis; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*tag= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gliese JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 195; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritis, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
XX
RESULT 806
ADMI4002/c
ID ADMI4002 standard; DNA; 20 BP.
XX
AC ADMI4002;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:189.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antidiabetic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b

FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
PS Claim 4; SEQ ID NO 189; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritis, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
XX
RESULT 807
ADMI4090/c
ID ADMI4090 standard; DNA; 20 BP.
XX
AC ADMI4090;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:277.
XX

KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key
FT modified_base
FT 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX
PS Claim 4; SEQ ID NO 277; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytosolic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX
XX Query March 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 808
ADM14151/c
ID ADM14151 standard; DNA; 20 BP.
XX
XX ADM14151;
XX
XX
DT 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:338.
XX
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key
FT modified_base
FT 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX
PS Claim 4; SEQ ID NO 338; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal

CC	having a disease or condition associated with mPGEs-1.
CC	mPGEs-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC	ophtalmic, immunologicl, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Fred. NO. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Oy	1520 AAAAAAAAAAGTAAAA 1537 Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 809	
ADM13997/c	
ID ADM13997 standard; DNA; 20 BP.	
XX ADM13997;	
AC	
XX	
D7 01-JUL-2004 (first entry)	
XX	
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:184.	
KM chimeric; antisense oligonucleotide; phosphorothioate; human;	
KM microosomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;	
KM microsomal prostaglandin E2 synthase inhibitor; cytosaratic; antidiabetic;	
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;	
KM neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;	
KM immunomodulatory; cardiovascular; gene therapy; inflammation;	
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;	
KM reperfusion injury; ophtalmic disorder; immunological disorder;	
KM cardiovascular disorder; neurological disorder; se.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT modified_base	1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	/tag= c
FT	/mod base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
W02004028458-A2.	
PN	
XX 08-APR-2004.	
XX	
PD	
XX	
PF 25-SEP-2003; 2003WO-US030374.	
XX	
PR 25-SEP-2002; 2002US-0413549P.	
XX	
PA (PHAA) PHARMACIA CORP.	
XX	
PI Gliese JK;	
XX	
WR WPI; 2004-305094/28.	

XX	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 184; 132pp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-10 bp targeted to a nucleic acid encoding
CC	mPGES-1, which specifically hybridize with the nucleic acid encoding
CC	mPGES-1 in cells or tissues; and (2) a method of inhibiting the expression of
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	be used for preparing a composition and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Oy	1520 AAAAAAAAAAAGTAAAA 1537
Db	20 AAAAAAAAAAAAAAAAAA 3
RESULT 810	
ADM14017/C	
ID	ADM14017 standard; DNA; 20 BP.
XX	
AC	ADM14017;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:204.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
PH	Location/Qualifiers
FT	1..20
FT	modified_base
FT	1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	modified_base
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	modified_base
FT	16..20
FT	/*tag= c

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FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese UK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 204; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The
XX human mpGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mpGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mpGES-1. mpGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mpGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mpGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 811
XX ADM14018/C
XX ID ADM14018 standard; DNA; 20 BP.
XX
XX AC ADM14018;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mpGES-1 chimeric antisense oligonucleotide SEQ ID NO.205.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mpGES-1; mpGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; cardiant; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
```

```
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20 /*tag= b
XX
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX modified_base 1..5 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX modified_base 16..20 /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese UK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 205; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The
XX human mpGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compound,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mpGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mpGES-1. mpGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mpGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mpGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 812
XX ADM14088/C
XX ID ADM14088 standard; DNA; 20 BP.
```

CC	ophthalmic, immunological, cardiovascular or neurological disorder.														
XX	Sequence	20	BP;	0	A;	0	C;	0	G;	20	T;	0	U;	0	Other;
XX	Query Match	1.1%; Score 14.8; DB 1; Length 20;													
XX	Best Local Similarity	88.9%; Pred.No. 4.4e+02;													
XX	Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;					
OY	1520	AAAAAAAAAAGTAAAA	1537												
DB	20	AAAAAAAAAAAAAAAAAAAA	3												
RESULT 813															
ADM14257/C															
ID	ADM14257	standard;	DNA;	20	BP.										
XX	AC	ADM14257;													
XX	DT	01-JUN-2004	(first entry)												
XX	XX	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:444.													
DE	XX	chimeric; antisense oligonucleotide; phosphorothioate; human;													
KM	XX	microsomal prostaglandin G2 synthase; mPGES-1; mPGES-1 inhibitor;													
KM	XX	microsomal prostaglandin G2 synthase inhibitor; cytosolic; antidiabetic;													
KM	XX	immunomodulator; cardiant; neuroprotective; antiinflammatory;													
KM	XX	neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;													
KM	XX	immunomodulatory; cardiovascular; gene therapy; inflammation;													
KM	XX	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;													
KM	XX	reperfusion injury; ophthalmic disorder; immunological disorder;													
KM	XX	cardiovascular disorder; neurological disorder; ss.													
OS	XX	Homo sapiens.													
OS	XX	Synthetic.													
FH	XX	Key	Location/Qualifiers												
FT	XX	modified_base	1..20												
FT	XX	FT	/*tag= b												
FT	XX	FT	/mod_base= OTHER												
FT	XX	FT	/note= "phosphorothioate linkages and all cytidine												
FT	XX	FT	residues are 5-methylcytidines"												
FT	XX	FT	1..5												
FT	XX	FT	/*tag= a												
FT	XX	FT	/mod_base= OTHER												
FT	XX	FT	/note= "2'-O-methoxyethyls"												
FT	XX	FT	16..20												
FT	XX	FT	/*tag= c												
FT	XX	FT	/mod_base= OTHER												
FT	XX	FT	/note= "2'-O-methoxyethyls"												
PN	XX	WO2004028458-A2.													
XX	XX	08-APR-2004.													
XX	XX	25-SEP-2003; 2003WO-US030374.													
XX	XX	25-SEP-2002; 2002US-0413549P.													
PA	XX	(PHAA) PHARMACIA CORP.													
PI	XX	Gierse JK;													
PI	XX	WPI; 2004-305094/28.													
DR	XX	New antisense compound, having a sequence targeted to a nucleic acid													
PT	XX	encoding mPGES-1, useful for preparing a composition for treating e.g.,													
PT	XX	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or													
PT	XX	ischemia.													
PS	XX	Claim 4; SEQ ID NO 444; 132pp; English.													
CC	The present sequence represents a chimeric antisense oligonucleotide														


```
FT modified_base      residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT modified_base
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 193; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
XX
XX Query Match      1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. NO. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX |||||||||
XX 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 816
XX ADM14014/c
XX ID ADM14014 standard; DNA; 20 BP.
XX
XX ADM14014;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:201.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
```

```
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX 1..20
XX modified_base
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX modified_base
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX 16..20
XX modified_base
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 201; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
XX
XX Query Match      1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. NO. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
```

```
Db          20 AAAAAAAAAAAAAAAAAA 3
|||||
RESULT 817
ADM14020/c
XX ADM14020 standard; DNA; 20 BP.
XX
AC ADM14020;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:207.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; cardiant; neuroprotective; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Glaxo JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX Claim 4; SEQ ID NO 207; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytosstatic.
```

```
CC anti diabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1520 AAAAAAAAAAGTAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
|||||
RESULT 818
ADM13991/c
XX ADM13991 standard; DNA; 20 BP.
XX
AC ADM13991;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:178.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Glaxo JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
```

PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
PS Claim 4; SEQ ID NO 178; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds;
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 819
ADM14003/C
ID ADM14003 standard; DNA; 20 BP.
XX
AC ADM14003;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:190.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key 1.20 Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT modified_base /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT modified_base /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

XX
XX W02004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PAAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 190; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds;
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 820
ADM14005/C
ID ADM14005 standard; DNA; 20 BP.
XX
AC ADM14005;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:192.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX Gliese JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 192; 132pp; English.
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX Query Match 1..13; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
Db 20 AAAAAAAAAAAAAAAAA 3
RESULT 821
ADM14246/c
ID ADM14246 standard; DNA; 20 BP.
XX
XX ADM14246;
AC
```

```
XX 01-JUL-2004 (first entry)
DT Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:433.
XX
XX DE
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX Gliese JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 433; 132pp; English.
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
```

```
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 822
ADM13995/C
ID ADM13995 standard; DNA; 20 BP.
XX
XX ADM13995;
XX
XX 01-JUL-2004. (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:182.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulator; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Glerse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX Claim 4; SEQ ID NO 182; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
```

```
CC 9g34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antiinflammatory, immunomodulator, cardiant, neuroprotective,
CC antidiabetic, immunomodulator, noctropic, neuroprotective,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
Db 20 AAAAAAAAAAAAAAAAA 3

RESULT 823
ADM14011/C
ID ADM14011 standard; DNA; 20 BP.
XX
XX ADM14011;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:198.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulator; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
```

XX	PI	(PhAA) PHARMACIA CORP.
XX	PI	Glerse JK;
XX	DR	WPI; 2004-305094/28.
XX	XX	
PT	PT	New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.
XX	XX	
PS	PS	Claim 4; SEQ ID NO 198; 132bp; English.
XX	XX	
CC	CC	The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. mPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antiinflammatory, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic, ophtalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophtalmic, immunological, cardiovascular or neurological disorder.
XX	XX	
XX	XX	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX	XX	
XX	XX	Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX	XX	Best Local Similarity 88.9%; Pred. NO. 4.4e+02;
XX	XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	Db	1520 AAAAAAAAAAGTAA 1537 20 AAAAAAAAAAAAAAAAA 3
XX	XX	
XX	XX	RESULT 824
AD	AD	ADML4240/C
XX	XX	ID ADML4240 standard; DNA; 20 BP.
XX	XX	ADML4240;
XX	XX	
XX	XX	01-JUN-2004 (first entry)
XX	XX	
DE	DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:427.
XX	XX	
KW	KW	chimeric; antisense oligonucleotide; phosphorothiate; human;
KW	KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	KW	microsomal prostaglandin E2 synthase inhibitor; cycostatic; antidiabetic;
KW	KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophtalmological;
KW	KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	KW	reperfusion injury; ophtalmic disorder; immunological disorder;
KW	KW	cardiovascular disorder; neurological disorder; ss.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	Synthetic.
XX	XX	
XX	XX	Key
FT	FT	Location/Qualifiers
FT	FT	modified_base 1..20
FT	FT	/*tag= b
FT	FT	/mod_base= OTHER
FT	FT	/note= "phosphorothiate linkages and all cytidine residues are 5-methylcytidines"
FT	FT	modified_base 1..5

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FT FT      /*tag= a
FT FT      /note= "2'-O-methoxyethyls"
FT FT      /tag= C
FT FT      /mod_base= OTHER
FT FT      /note= "2'-O-methoxyethyls"
XX XX
XX XX      NO2004028458-A2.
XX XX
XX XX      08-APR-2004.
XX XX
XX XX      25-SEP-2003; 2003WO-US030374.
XX XX
XX XX      25-SEP-2002; 2002US-0413549P.
XX XX
XX XX      (PHAA ) PHARMACIA CORP.
XX XX
XX XX      Glaser JK;
XX XX
XX XX      WPI; 2004-305094/28.
XX XX
XX XX      New antisense compound, having a sequence targeted to a nucleic acid
PT PT      encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT PT      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT PT      ischemia.
XX XX
XX XX      Claim 4; SEQ ID NO 427; 132pp; English.
XX XX
XX XX      The present sequence represents a chimeric antisense oligonucleotide
CC CC      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC CC      human mPGES-1 gene is located on chromosome 9, more specifically to
CC CC      9q34.3. The present invention also describes: (1) antisense compounds,
CC CC      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC CC      mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC CC      inhibit its expression; (2) a method of inhibiting the expression of
CC CC      mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC CC      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC CC      antisense oligonucleotides and antisense compounds have cyrotatic,
CC CC      antidiabetic, immunomodulator, cardiant, neuroprotective,
CC CC      antiinflammatory, neuroprotective, nootropic, antarthritic, vasotropic,
CC CC      ophthalmological, immunomodulatory and cardiovascular activities, and can
CC CC      be used as mPGES-1-inhibitors and in gene therapy. The antisense compound
CC CC      can be used for preparing a composition for treating a disease or
CC CC      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC CC      disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC CC      ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ SQ
SQ SQ      Query Match 1.1%; Score 14.8; DB 1; Length 20;
SQ SQ      Best local Similarity 88.9%; Pred. No. 4.4e+02;
SQ SQ      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX XX
XX XX      1520 AAAAAAAAAAAGTAAA 1537
XX XX      |||||
XX XX      |||||
XX XX      |||||
XX XX      20 AAAAAAAAAAAAAAAA 3
XX XX
XX XX
XX XX
XX XX      ADML14009;
XX XX
XX XX      01-JUL-2004 (first entry)
XX XX
XX XX      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:196.
XX XX
XX XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
XX XX      microsomal prostaglandin E2 synthase inhibitor; cyrotatic; antidiabetic;
XX XX      immunomodulator; cardiant; neuroprotective; antiinflammatory;

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KV		immunoprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW		immunomodulatory; cardiovascular; gene therapy; inflammation;
KX		Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KY		reperfusion injury; ophthalmic disorder; immunological disorder;
KZ		cardiovascular disorder; neurological disorder; ss.
XX		
OS		Homo sapiens.
OS		Synthetic.
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "phosphorothionate linkages and all cytidine residues are 5-methylcytidines"
FT	modified_base	1..5
FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
FT	modified_base	16..20
FT		/tag= C
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
XX		
PN	WO2004028458-A2.	
PD	08-APR-2004.	
PF	25-SEP-2003; 2003WO-US030374.	
PR	25-SEP-2002; 2002US-0433549P.	
PA	(PHAA) PHARMACIA CORP.	
PI	Gierse JK;	
PJ	WPI; 2004-305094/28.	
PT	New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.	
PS	Claim 4; SEQ ID NO 196; 132pp; English.	
XX		
CC	The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q24.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. mPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:	
QY	Query Match	1.1%; Score 14.8; DB 1; Length 20;
	Best Local Similarity	88.9%; Pred. No. 4,4e+02;
DB	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
	1520 AAAAAAAAAAAGTAAA 1537	
	20 AAAAAAAAAAAAAAAAAA 3	

RESULT 826	
ADML4010/c	
ID	ADML4010 standard; DNA; 20 BP.
XX	
AC	
XX	ADML4010;
DT	
XX	01-JUL-2004 (first entry)
DE	
XX	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:197.
XX	
XX	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic
KW	immunomodulator; cardiatic; neuroprotective; antiinflammatory;
KW	neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	modified_base
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	modified_base
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
PN	WO2004028458-A2.
XX	
XX	
PD	08-APR-2004.
XX	
XX	
PF	25-SEP-2003; 2003WO-US030374.
XX	
PR	25-SEP-2002; 2002US-0413549P.
XX	
PA	(PHAA) PHARMACIA CORP.
XX	
XX	
PI	Gierse JK;
DR	WPI; 2004-305094/28.
XX	
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
BS	Claim 4; SEQ ID NO 197; 132p; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiatic, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,

CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1520 AAAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 827
ADM14089/C
ID ADM14089 standard; DNA; 20 BP.
XX
AC ADM14089;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:276.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*tag= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX
XX PD 08-APR-2004.
XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX
XX PA (PHAA) PHARMACIA CORP.
XX
XX PI Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT

PT ischaemia.
XX
XX Claim 4; SEQ ID NO 276; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1520 AAAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 828
ADM14016/C
ID ADM14016 standard; DNA; 20 BP.
XX
AC ADM14016;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:203.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*tag= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX

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XX 08-APR-2004.
PD modified_base 1..20
PP 25-SEP-2003; 2003WO-US030374.
PR 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
PA
XX
PI Gliese JK;
XX
XX WPI; 2004-305094/28.
DR
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
PS
XX Claim 4; SEQ ID NO 203; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridize with the nucleic acid mPGEs-1 and
CC inhibit its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 829
ADMI4075/C
ID ADMI4075 standard; DNA; 20 BP.
XX
XX ADMI4075;
AC
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:262.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
```

```
PH Key Location/Qualifiers
PT modified_base 1..20
PT /+tag= b
PT /mod_base= OTHER
PT /note= "phosphorothioate linkages and all cytidine
PT residues are 5-methylcytidines"
PT modified_base 1..5
PT /*tag= a
PT /mod_base= OTHER
PT /note= "2'-O-methoxyethyls"
PT modified_base 16..20
PT /*tag= c
PT /mod_base= OTHER
PT /note= "2'-O-methoxyethyls"
PN W02004028458-A2.
XX
XX 08-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030374.
PP
XX
XX 25-SEP-2002; 2002US-0413549P.
PR
XX
XX (PHAA ) PHARMACIA CORP.
PA
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
DR
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
PS
XX Claim 4; SEQ ID NO 262; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridize with the nucleic acid mPGEs-1 and
CC inhibit its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 830
ADMI4189/C
ID ADMI4189 standard; DNA; 20 BP.
XX
XX ADMI4189;
AC
XX
XX 01-JUL-2004 (first entry)
XX
```

```

XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:376.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX Key
XX modified_base
XX 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 376; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mpGS-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mpGS-1. mpGS-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytosolic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory, and cardiovascular activities, and can
XX be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mpGS-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

```

```

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 831
ADM13996/C
ID ADM13996 standard; DNA; 20 BP.
AC
XX ADM13996;
XX
XX 01-JUL-2004 (first entry)
XX
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:183.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key
XX Location/Qualifiers
XX 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 183; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding

```

CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunologic, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 832
ADM14001/C
ID ADM14001 standard; DNA; 20 BP.
XX
AC ADM14001;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:188.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1..20
FT Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX

PI Gierse JK;
XX
XX WPI; 2004-305094/28.
DR
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGEs-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX Claim 4; SEQ ID NO 188; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
XX human mPGEs-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGEs-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 833
ADM14004/C
ID ADM14004 standard; DNA; 20 BP.
XX
AC ADM14004;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:191.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1..20
FT Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
XX
XX

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FT modified_base /note= "2'-O-methoxyethyls"
FT 16.20
FT /*tag= C
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 191; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAA 1537
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 834
XX ADM14012/C
XX ID ADM14012 standard; DNA; 20 BP.
XX
XX AC ADM14012;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:199.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;

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XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /*note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /*note= "2'-O-methoxyethyls"
XX
XX modified_base 16..20
XX /*tag= C
XX /mod_base= OTHER
XX /*note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 191; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAA 1537
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX

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RESULT 835
ADM14467/C
ID ADM14467 standard; DNA; 20 BP.
XX
AC ADM14467;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin H2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin H2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotrophic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 654; 132p; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin H2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
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```
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC opthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX 18 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 836
ADM14015/C
ID ADM14015 standard; DNA; 20 BP.
XX
AC ADM14015;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:202.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin H2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin H2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotrophic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
```

PS Claim 4; SEQ ID NO 202; 132pp; English.

XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3

RESULT 837
ADM14021/c
ID ADM14021 standard; DNA; 20 BP.

XX
AC ADM14021;

DT 01-JUL-2004 (first entry)

XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:208.

XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.

XX
OS Homo sapiens.

OS Synthetic.

XX
FH Key Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX 08-APR-2004.

XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.

XX
PS Claim 4; SEQ ID NO 208; 132pp; English.

XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3

RESULT 838
ADM14388/c
ID ADM14388 standard; DNA; 20 BP.

XX
AC ADM14388;

DT 01-JUL-2004 (first entry)

XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:575.

XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.

XX
OS Homo sapiens.

OS Synthetic.

XX
FH Key Location/Qualifiers
FT 1..20
FT modified_base
XX
XX


```
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "phosphorothioate linkages and all cytidine
FT      residues are 5-methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
PN      WO2004028458-A2.
PD      08-APR-2004.
PP      25-SEP-2003; 2003WO-US030374.
PR      25-SEP-2002; 2002US-0413549P.
PX      (PHMA ) PHARMACIA CORP.
PI      Gliese JK;
PI      MPI; 2004-305094/28.
DR      MPI; 2004-305094/28.
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX      ischemia.
XX      Claim 4; SEQ ID NO 575; 132pp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
XX      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX      human mPGES-1 gene is located on chromosome 9, more specifically to
XX      9q34.3. The present invention also describes: (1) antisense compounds,
XX      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX      mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX      inhibits its expression; (2) a method of inhibiting the expression of
XX      mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX      antisense oligonucleotides and antisense compounds have cytostatic,
XX      antidiabetic, immunomodulator, cardiant, neuroprotective, vasotropic,
XX      antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX      CC antiinflammatory, immunomodulatory and cardiovascular activities, and can
XX      be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX      CC can be used for preparing a composition for treating a disease or
XX      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX      CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1520 AAAAAAAAAAGTAAA 1537
Db      20 AAAAAAAAAAAAAAAAAA 3
RESULT 839
ADM14013/C
ID      ADM14013 standard; DNA; 20 BP.
XX
XX      ADM14013;
XX
XX      01-JUL-2004 (first entry)
XX
XX      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:200.
```

```
XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
KW      microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW      microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW      immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW      neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW      immunomodulatory; cardiovascular; gene therapy; inflammation;
KW      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW      reperfusion injury; ophthalmic disorder; immunological disorder;
KW      cardiovascular disorder; neurological disorder; ss.
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
FH      modified_base
FT      1. .20
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "phosphorothioate linkages and all cytidine
FT      residues are 5-methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
XX      WO2004028458-A2.
XX      08-APR-2004.
XX      25-SEP-2003; 2003WO-US030374.
XX      25-SEP-2002; 2002US-0413549P.
XX      (PHMA ) PHARMACIA CORP.
XX      Gliese JK;
XX      MPI; 2004-305094/28.
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX      ischemia.
XX      Claim 4; SEQ ID NO 200; 132pp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
XX      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX      human mPGES-1 gene is located on chromosome 9, more specifically to
XX      9q34.3. The present invention also describes: (1) antisense compounds,
XX      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX      mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX      inhibits its expression; (2) a method of inhibiting the expression of
XX      mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX      antisense oligonucleotides and antisense compounds have cytostatic,
XX      antidiabetic, immunomodulator, cardiant, neuroprotective,
XX      CC antiinflammatory, immunomodulatory and cardiovascular activities, and can
XX      be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX      CC can be used for preparing a composition for treating a disease or
XX      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX      CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
```

```
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 840
ADM14019/c
ID ADM14019 standard; DNA; 20 BP.
XX
XX ADM14019;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:206.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opthalamic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX PI
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX
XX Claim 4; SEQ ID NO 206; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
```

```
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytosolic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC opthalamic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 841
ADM14087/c
ID ADM14087 standard; DNA; 20 BP.
XX
XX ADM14087;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:274.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opthalamic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX PI
```

DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 274; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antiinflammatory, neuroprotective, cardiant, neuroprotective,
CC ophthalmological, immunomodulatory, and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 842
ADM14300/c
ID ADM14300 standard; DNA; 20 BP.
XX
AC ADM14300;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:487.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; cardiant; neuroprotective; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
FH
FT Key Location/Qualifiers
FT 1..20
FT /mod bases= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod bases= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20

FT /*tag= c
FT /mod bases= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK.
XX
XX WPI; 2004-305094/28.
XX
DR
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 487; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antiinflammatory, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, cardiant, neuroprotective,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 843
ADM13993/c
ID ADM13993 standard; DNA; 20 BP.
XX
AC ADM13993;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:180.
XX
KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; cardiant; neuroprotective; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;

KW		cardiovascular disorder; neurological disorder; ss.
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "phosphorochiate linkages and all cytidine residues are 5-methylcytidines"
FT	modified_base	1..5
FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
FT	modified_base	16..20
FT		/tag= c
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
PN	WO200402845B-A2.	
PD	08-APR-2004.	
PP	25-SEP-2003; 2003WO-US030374.	
PR	25-SEP-2002; 2002US-0413549P.	
PA	(PHAA) PHARMACIA CORP.	
PI	Gierse JK;	
XX		
DR	WPI; 2004-305094/28.	
PT	New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.	
PT		
PS	Claim 4; SEQ ID NO 180; 132bp; English.	
XX		
CC	The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin H ₂ synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q44.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. mPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulatory, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophtalmic, immunological, cardiovascular or neurological disorder.	
XX		
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;	
	Query Match 1.1%; Score 14.8; DB 1; Length 20;	
	Best Local Similarity 88.9%; Pred. No. 4.4e+02;	
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.	
OY	1520 AAAAAAAAAAAGTAAA 1537 Db 20 AAAAAAAAAAAAAAA 3	
RESULT 844		
ADMI3J98/C		

ID	ADM13998	standard; DNA; 20 BP.
XX	AC	ADM13998;
XX	DT	01-JUL-2004 (first entry)
XX	DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:185.
KW	KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	KW	microsomal prostaglandin E2 synthase inhibitor; cyclooxygenase; antidiabetic;
KW	KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW	KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	KW	cardiovascular disorder; neurological disorder; ss.
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	FT	Key
XX	FT	Location/Qualifiers
XX	FT	modified_base
XX	FT	1..20
XX	FT	/*tag= b
XX	FT	/mod_base= OTHER
XX	FT	/note= "phosphorothioate linkages and all cytidine
XX	FT	residues are 5-methylcytidines"
XX	FT	modified_base
XX	FT	1..5
XX	FT	/*tag= a
XX	FT	/mod_base= OTHER
XX	FT	/note= "2',-O-methoxyethyls"
XX	FT	modified_base
XX	FT	16..20
XX	FT	/*tag= c
XX	FT	/mod_base= OTHER
XX	FT	/note= "2',-O-methoxyethyls"
XX	PN	NO2004028458-A2.
XX	PD	08-APR-2004.
XX	XX	
XX	XX	25-SEP-2003; 2003WO-US030374.
XX	XX	
XX	XX	25-SEP-2002; 2002US-0413549P.
XX	PR	
XX	PA	(PHAA) PHARMACIA CORP.
XX	PA	
XX	P1	Glesee JK;
XX	P1	
XX	WI	WIPI; 2004-305094/28.
DR	XX	
XX	XX	New antisense compound, having a sequence targeted to a nucleic acid
XX	XX	encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX	XX	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX	XX	ischemia.
PS	PS	Claim 4; SEQ ID NO 185; 132pp; English.
XX	XX	
XX	XX	The present sequence represents a chimeric antisense oligonucleotide
CC	CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	CC	mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC	CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	CC	antisense oligonucleotides and antisense compounds have cyclostatic,
CC	CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	CC	antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC	CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC	CC	can be used for preparing a composition for treating a disease or
CC	CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's

CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 845
ADM14007/C
ID ADM14007 standard; DNA; 20 BP.
XX
AC ADM14007;
XX
DT 01-JUL-2004 (first entry)
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:194.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
FN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PP 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PMDA) PHARMACTA CORP.
XX
PI Glaxo JK;
XX
DR WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 194; 132pp; English.
XX

CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 846
ADM14124/C
ID ADM14124 standard; DNA; 20 BP.
XX
AC ADM14124;
XX
DT 01-JUL-2004 (first entry)
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:311.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
FN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PP 25-SEP-2003; 2003WO-US030374.
XX

XX	25-SEP-2002; 2002US-0413549P.
XX	(PHAA) PHARMACIA CORP.
PA	
XX	Gliese JK;
PI	
XX	WPI, 2004-305094/28.
DR	
XX	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
PS	Claim 4; SEQ ID NO 311; 1322p; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	9q44.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC	cardiovascular, immunomodulatory and cardiovascular activities, and can
CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
SO	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
QY	Query Match 1.1%; Score 14.8; DB 1; Length 20;
	Best Local Similarity 88.9%; Pred. No. 4.4e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
DB	1520 AAAAAAAAAAGTAAA 1537
	20 AAAAAAAAAAAAAAAAAA 3
RESULT 847	
ADM14216/C	
ID	ADM14216 standard; DNA; 20 BP.
AC	ADM14216;
XX	
DT	01-JUN-2004 (first entry)
XX	
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:403.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cyostatic; antidiabetic;
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	Location/Qualifiers
FT	Key 1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	

[illegible]

KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX Homo sapiens.
 XX US2004049022-A1.
 XX 11-MAR-2004.
 XX 25-JUL-2003; 2003US-00627930.
 XX 23-APR-2002; 2002WO-US013135.
 XX 23-APR-2002; 2002WO-US013143.
 XX (NYCE/) NYCE J W.
 XX (SAND/) SANDRASAGRA A.
 XX (TANG/) TANG L.
 XX (AGUI/) AGUILAR D.
 XX (MILL/) MILLER S.
 XX (SHAH/) SHAHABUDDIN S.
 XX (LUTH/) LU H.
 XX (CONG/) CONG H.
 XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 XX Shahabuddin S, Lu H, Cong H;
 XX WPI; 2004-293804/27.
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 XX asthma.
 XX Claim 2; SEQ ID NO 1791; 174bp; English.
 XX The invention relates to oligonucleotides anti-sense to an initiation
 XX codon, coding region, 5' or 3' intron-exon junction, intron or region
 XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 XX -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 XX also relates to a method of screening a candidate compound that binds to
 XX one or more nucleic acid target(s) or expressed product(s), for the
 XX prevention and/or treatment of a respiratory or lung disease. The
 XX oligonucleotides are useful for reducing or inhibiting expression of a
 XX gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 XX CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 XX tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 XX useful for preventing or treating a respiratory or lung disease. The
 XX respiratory or lung disease is associated with hyper-responsiveness to
 XX and/or increased levels of, adenosine and/or levels of adenosine A
 XX receptor(s), and/or asthma and/or lung allergies associated with
 XX inflammation or an inflammatory disease. The respiratory or lung disease
 XX is chosen from airway inflammation, allergy, asthma, impeded respiration,
 XX cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 XX allergic rhinitis, acute respiratory distress syndrome, pulmonary
 XX hypertension, lung inflammation, bronchitis, airway obstruction or
 XX bronchoconstriction. This sequence represents an oligonucleotide of the
 XX invention.
 XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAAA 1537

Db 19 AAAAAAAAAAAAAAAAAA 2
 RESULT 849
 ID ADO03711 standard; DNA; 20 BP.
 AC ADO03711;
 DT 29-JUL-2004 (first entry)
 DE SERS-based analyte detection oligonucleotide seqid 31.
 KW Raman label; specific binding member; surface-enhanced Raman scattering;
 KW SERS; ss.
 OS Synthetic.
 XX US2004086897-A1.
 XX 06-MAY-2004.
 XX 07-MAY-2003; 2003US-00431341.
 XX 07-MAY-2002; 2002US-0378538P.
 XX 28-MAY-2002; 2002US-0383630P.
 XX 14-JUN-2002; 2002US-00172428.
 XX (MIRK/) MIRKIN C A.
 XX (CAOY/) CAO Y.
 XX (JINR/) JIN R.
 XX Mirkin CA, Cao Y, Jin R;
 XX WPI; 2004-418413/39.
 XX Reagent, useful for detecting target analyte e.g., nucleic acid,
 XX comprising particle having bound to at least one Raman label, which can
 XX be activated to provide surface-enhanced Raman scattering effect, and
 XX specific binding member.
 XX Disclosure; SEQ ID NO 31; 55bp; English.
 XX The invention describes a reagent (I) comprising a particle bound to at
 XX least one Raman label and a specific binding member, where the Raman
 XX label can be activated to provide a surface-enhanced Raman scattering
 XX (SERS) effect or comprising a specific binding member having two or more
 XX different Raman labels bound to it. Also described are: a test kit (II),
 XX comprising (I) in one container and a silver, gold or copper Raman
 XX enhancer stain in another container; and a fibre optic detection device
 XX (III), having a bundle of optical fibres terminating with ends of the
 XX optical fibre, where a several of the optical fibres have (I) located at
 XX the ends of the optical fibre. (I) is useful for: detecting for the
 XX presence or absence of one or more target analytes in a sample, the
 XX target analytes having at least two binding sites; detecting the presence
 XX or absence of one or more target nucleic acid in a sample, the sequence
 XX of the nucleic acid having at least two portions; and for screening one
 XX or more molecules to determine whether the molecule is a ligand to one or
 XX more specific receptors. This sequence represents an oligonucleotide
 XX associated with the SERS-based detection analyte detection method.
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAAA 1537
 1 AAAAAAAAAAAAAAAAAA 18


```
RESULT 850
ADP78301/c
XX ADP78301 standard; DNA; 20 BP.
XX
AC ADP78301;
XX
XX 12-AUG-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide #2100.
XX
XX GFAT; Antidiabetic; Cardiant;
XX Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
XX repertusion; ss.
XX
XX Synthetic.
XX
XX Key location/Qualifiers
XX modified_base 1..4
XX /*cag= a
XX /mod_base= other
XX /note= "2-methoxyethyl wing"
XX modified_base 17..20
XX /*cag= b
XX /mod_base= other
XX /note= "2-methoxyethyl wing"
XX
XX WO2004035763-A2.
XX
XX 29-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US033332.
XX
XX 17-OCT-2002; 2002US-0419268P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Broeschat KO, Crosby SD;
XX
XX WPI; 2004-348453/32.
XX
XX New compound, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX ischemia/repertusion injury.
XX
XX Claim 4; SEQ ID NO 2100; 175pp; English.
XX
XX The present invention relates to a compound which specifically hybridizes
XX with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX modulating the expression of GFAT, and which comprise any of the 3063
XX sequences of 20 base pairs, given in the specification. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX cardiovascular or neurological disorder, ischemia/repertusion injury.
XX They are also useful in research and diagnosis for modulating the
XX expression of GFAT. The present sequence represents a chimeric
XX phosphorothioate oligonucleotide with 2'-MOB wings and a deoxy gap, these
XX oligonucleotides inhibit human GFAT expression.
XX
XX Sequence 20 BP; 11 A; 1 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1252 TTTTGTGTTTAAATCAGA 1265
DB 20 TTTTGTGTTTAAATCAGA 3
```

RESULT 851
ADP10746

```
ID ADP10746 standard; DNA; 20 BP.
XX
XX AC ADP10746;
XX
XX 12-AUG-2004 (first entry)
XX
XX Set 1 Left PCR primer for marker probe #91.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Mehlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX
XX Claim 58; SEQ ID NO 755; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection.
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
XX of allograft rejection and other disorders.
XX
XX Sequence 20 BP; 0 A; 3 C; 8 G; 9 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 545 TGTGTGCTGTGTGCGTG 562
DB 1 TGTGTGCTGTGTGCGTG 18
```

RESULT 852
ADP20152
ID ADP20152 standard; DNA; 20 BP.
XX
XX AC ADP20152;
XX
XX 26-AUG-2004 (first entry)
XX
XX Nucleic acid detection method linking oligonucleotide #66.
XX
XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;

```
KW genetic disease; bacterial infection; viral infection; forensic;
KW DNA sequencing; paternity testing; linking oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004110220-A1.
XX
PD 10-JUN-2004.
XX
PF 18-NOV-2003; 2003US-00716829.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z;
XX
DR WPI: 2004-440357/41.
XX
PT Nanoparticles useful for detection and separation of nucleic acids e.g.
PT genes associated with disease, in a diagnostic assay, comprise several
PT oligonucleotides attached to them.
XX
PS Example 24; SEQ ID NO 70; 142pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. The method is used for detection and separation
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA
CC from biological sources or PCR products) for diagnosis of various
CC diseases (such as genetic diseases, bacterial infections and viral
CC infections) and for forensics, DNA sequencing, paternity testing and
CC monitoring gene therapy. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 853
ADP20137
ID ADP20137 standard; DNA; 20 BP.
XX
AC ADP20137;
XX
DT 26-AUG-2004 (first entry)
DE Nucleic acid detection method linking oligonucleotide #54.
XX
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
```

```
KW genetic disease; bacterial infection; viral infection; forensic;
KW DNA sequencing; paternity testing; linking oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004110220-A1.
XX
PD 10-JUN-2004.
XX
PF 18-NOV-2003; 2003US-00716829.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z;
XX
DR WPI: 2004-440357/41.
XX
PT Nanoparticles useful for detection and separation of nucleic acids e.g.
PT genes associated with disease, in a diagnostic assay, comprise several
PT oligonucleotides attached to them.
XX
PS Example 18; SEQ ID NO 55; 142pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. The method is used for detection and separation
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA
CC from biological sources or PCR products) for diagnosis of various
CC diseases (such as genetic diseases, bacterial infections and viral
CC infections) and for forensics, DNA sequencing, paternity testing and
CC monitoring gene therapy. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 854
ADP69379/C
ID ADP69379 standard; DNA; 20 BP.
XX
AC ADP69379;
XX
DT 09-SEP-2004 (first entry)
DE Human mltONEBT-specific antisense oligonucleotide #273.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
```

```
KM insulin sensitising antidiabetic thiazolidinediones; mitonERT; diabetes;
KM immunological disorder; cardiovascular disorder; including hypertension;
KM neurological disorders; ischaemia; reperfusion; ss;
KM 2'-methoxyethyl gapper; 2'-MOE gapper; phosphorothioate backbone.
OS Homo sapiens.
XX
XX WO2004053060-A2.
XX
XX 24-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037621.
XX
XX 06-DEC-2002; 2002US-0431529P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Colca JR;
XX
XX WPI; 2004-468836/44.
XX
XX
XX New antisense oligonucleotides encoding mitonERT, useful for modulating
PT mitonERT expression or for treating diseases associated with mitonERT,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
XX Claim 4; SEQ ID NO 273; 226pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolidinediones (referred to as: mitonERT). The antisense
CC oligonucleotides of the invention are useful for modulating mitonERT
CC expression and for treating diseases or conditions associated with
CC mitonERT, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitonERT-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapper with a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 3 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 TTAATTAAAAA 1531
DB 19 TTAACAAAAA 2
RESULT 855
ADP69506/C
ID ADP69506 standard; DNA; 20 BP.
AC
XX ADP69506;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human mitonERT-specific antisense oligonucleotide #400.
DE
XX human; antisense oligonucleotide; mitochondrial membrane;
KM insulin sensitising antidiabetic thiazolidinediones; mitonERT; diabetes;
KM immunological disorder; cardiovascular disorder; including hypertension;
KM neurological disorders; ischaemia; reperfusion; ss;
KM 2'-methoxyethyl gapper; 2'-MOE gapper; phosphorothioate backbone.
XX
XX Homo sapiens.
XX
XX WO2004053060-A2.
XX
XX 24-JUN-2004.
XX
XX
```

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PF 25-NOV-2003; 2003WO-US037621.
XX
XX 06-DEC-2002; 2002US-0431529P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Colca JR;
XX
XX WPI; 2004-468836/44.
XX
XX
XX New antisense oligonucleotides encoding mitonERT, useful for modulating
PT mitonERT expression or for treating diseases associated with mitonERT,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
XX Claim 4; SEQ ID NO 400; 226pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolidinediones (referred to as: mitonERT). The antisense
CC oligonucleotides of the invention are useful for modulating mitonERT
CC expression and for treating diseases or conditions associated with
CC mitonERT, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitonERT-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapper with a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 TTAATTAAAAA 1531
DB 18 TTAACAAAAA 1
RESULT 856
ADQ80728/C
ID ADQ80728 standard; DNA; 20 BP.
AC
XX ADQ80728;
XX
XX 23-SEP-2004 (first entry)
XX
XX Porcine TSSCS intron 1 DN-primer.
DE
XX Anorectic; Antidiabetic; Muscular; Gene Therapy; Cpg island;
KM IGF2 gene intron 3; muscle mass; fat deposition; test number; obesity;
KM muscle deficiency; diabetes; PCR; primer; ss; pig.
XX
XX Sus scrofa.
XX
XX EP1437418-A1.
XX
XX 14-JUL-2004.
XX
XX 10-JAN-2003; 2003EP-00075091.
XX
XX 10-JAN-2003; 2003EP-00075091.
XX
XX (UYLT-) UNIV LIEGE.
XX (MELI-) MELICA HB.
XX (GENT-) GENTEC BV.
XX
XX Andersson L, Andersson G, Georges M, Buys N;
XX
XX WPI; 2004-501307/48.
XX
XX Selecting an animal for desired genotypic or potential phenotypic
PT
```

PT properties such as muscle mass and/or fat deposition, comprises testing
PT for a single nucleotide polymorphism in intron 3 of the IGF2 gene.
XX
PS Example 1, Page 20, 38pp; English.
XX
XX The present invention relates to a method (M1) for selecting an animal
XX for having desired genotypic or potential phenotypic properties. (M1)
XX comprises testing the animal for the presence of a nucleic acid
XX modification affecting the activity of an evolutionarily conserved Cpg
XX island located in intron 3 of an IGF2 gene, and/or binding of a nuclear
XX factor to an IGF2 gene. The nuclear factor is capable of binding to a
XX stretch of nucleotides which in the wild type pig, mouse or human IGF2
XX gene is part of an evolutionarily conserved Cpg island, located in intron 3
XX of the IGF2 gene. The stretch is functionally equivalent to (AD080709).
XX The nucleic acid modification in AD080709 comprises a G to A transition
XX at IGF2-intron3-nt3072. (M1) is useful for selecting an animal with
XX properties related to muscle mass, fat deposition, and/or test number.
XX Also claimed is a method (M2) for modulating mRNA transcription of an
XX IGF2 gene by modulating the activity of an evolutionarily conserved Cpg
XX island located in intron 3 of an IGF2 gene and/or modulating binding of a
XX nuclear factor to an IGF2 gene. Also claimed is a method (M3) for
XX identifying a compound capable of modulating mRNA transcription of an
XX IGF2 gene and a method (M4) for identifying a compound capable of
XX modulating binding of a nuclear factor to an IGF2 gene. (M2) is useful
XX for modulating mRNA transcription of an IGF2 gene in a cell or organism.
XX (M3) and (M4) are useful for identifying compounds capable of modulating
XX mRNA transcription of an IGF2 gene and/or modulating binding of a nuclear
XX factor to an IGF2 gene. Compounds identified are potentially useful for
XX treating obesity, muscle deficiencies and diabetes. The present sequence
XX is a primer which was used to produce porcine sequence tagged sites (STS)
XX in an example from the invention.
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 651 GCCGAGCGCGCTCAGAC 668
Db 19 GCCGATGCGCTCAGAC 2
RESULT 857
ADP99304/C ID ADP99304 standard; DNA; 20 BP.
XX
XX AC ADP99304;
XX DT 23-SEP-2004 (first entry)
XX
XX Stem cell factor, SCF, universal PCR primer #4.
XX
XX SCF, stem cell factor; gene therapy; haematopoietic progenitor cell;
XX aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
XX myelocleatosis; osteopetrosis; metastatic carcinoma; acute leukaemia;
XX multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
XX Niemann-Pick disease; Letterer-Siwe disease;
XX refractory erythroidlastic anaemia; Di Guglielmo syndrome;
XX congestive splenomegaly; kala awar; sarcoidosis;
XX primary splenic pancytopenia;iliary tuberculousis;
XX disseminated fungus disease; Fulminating septicemia; malaria;
XX Vitamin B12 deficiency; follic acid deficiency; pyridoxine deficiency;
XX Diamond Blackfan anaemia; hypopigmentation disorder; plealdism;
XX vitiligo; neurological damage; infertility; intestinal damage;
XX irradiation; chemotherapy; AIDS; haematopoietic recovery;
XX acute blood loss; neoplasm; cancer; ss; PCR; primer.
XX
XX Mammalia.
XX
XX US6759215-B1.
XX
XX 06-JUL-2004.

XX
PF 07-AUG-2000; 2000US-00635251.
XX
XX
XX 16-OCR-1989; 89US-00423283.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCR-1990; 90US-00589701.
XX 10-APR-1991; 91US-00684535.
XX 25-NOV-1992; 92US-00982225.
XX 21-DEC-1993; 93US-00172329.
XX 24-MAY-1995; 95US-00449182.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2004-497128/47.
XX
XX
XX Preparing a human stem cell factor (SCF) polypeptide, useful for treating
XX hematopoietic disorders, e.g., aplastic anemia, comprises growing host
XX cells transformed or transfected with DNA encoding a human SCF.
XX
XX Example 3; SEQ ID NO 34; 210pp; English.
PS
XX
XX The invention relates to preparing a (vertebrate) human stem cell factor
XX (SCF) polypeptide comprising growing host cells transformed or
XX transfected with DNA encoding a human SCF that stimulates growth of
XX haematopoietic progenitor cells under nutrient conditions, the DNA being
XX operatively linked to an expression control sequence, and isolating the
XX polypeptide produced. Also included is a recombinant host cell
XX transformed or transfected with an expression construct comprising a
XX vertebrate SCF polypeptide-encoding DNA operatively linked to a
XX heterologous expression regulatory sequence, permitting the expression of
XX the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat
XX and human nucleic acids encoding SCF, SCF proteins from a number of other
XX mammals and recombinantly expressed SCF protein fragments. The DNA
XX sequences are useful for effecting the large scale synthesis of SCF by a
XX variety of recombinant techniques or for generating new and useful viral
XX and circular plasmid DNA vectors, new and useful transformed and
XX transfected prokaryotic and eukaryotic host cells, and new and useful
XX methods for cultured growth of such host cells capable of expression of
XX SCF and its related products. The DNA sequences are also useful as
XX labelled probes in isolating human genomic DNA encoding SCF, in methods
XX of protein synthesis, in genetic therapy in humans and other mammals, and
XX in developing transgenic mammalian species which may serve as eukaryotic
XX hosts for production of SCF and SCF products in quantity. The SCF is
XX useful for treating haematopoietic disorders, e.g., aplastic anaemia,
XX paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelocleatosis,
XX osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
XX Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
XX Letterer-Siwe disease, refractory erythroidlastic anaemia, Di Guglielmo
XX syndrome, congestive splenomegaly, kala awar, sarcoidosis, primary
XX splenic pancytopenia,iliary tuberculousis, disseminated fungus disease,
XX fulminating septicemia, malaria, vitamin B 12 and follic acid deficiency,
XX pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
XX disorders such as plebaldism and vitiligo. The SCF are also useful for
XX treating neurological damage, infertility states, intestinal damage
XX resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
XX for enhancing hematopoietic recovery after acute blood loss and as a
XX boost to the immune system for fighting neoplasia (cancer). The present
XX sequence is a universal SCF PCR primer used in the isolation of SCF DNA.
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 858
ADP99302/c
ID ADP99302 standard; DNA; 20 BP.
XX
AC ADP99302;
XX
DT 23-SEP-2004 (first entry)
XX
DE Stem cell factor, SCF, universal PCR primer #2.
XX
KM SCF, stem cell factor; gene therapy; haematopoietic progenitor cell;
KM aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
KM myelocleiosis; osteopetrosis; metastatic carcinoma; acute leukaemia;
KM multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
KM Niemann-Pick disease; Letterer-Siwe disease;
KM refractory erythroidlastic anaemia; Di Guglielmo syndrome;
KM congenitive splenomegaly; Kala awar; sarcoidosis;
KM primary splenic pancytopenia; miliary tuberculosis;
KM disseminated fungus disease; fulminating septicemia; malaria;
KM vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;
KM Diamond Blackfan anaemia; hypopigmentation disorder; plebaldism;
KM vitiligo; neurological damage; infertility; intestinal damage;
KM irradiation; chemotherapy; AIDS; haematopoietic recovery;
KM acute blood loss; neoplasm; cancer; ss; PCR; primer.
XX
OS Mammalia.
XX
PN US6759215-B1.
XX
PD 06-JUL-2004.
XX
PF 07-AUG-2000; 2000US-00635251.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449182.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zeebo XM, Boseelman RA, Suggs SV, Martin FH;
PI WPI; 2004-497128/47.
XX
PT Preparing a human stem cell factor (SCF) polypeptide, useful for treating
PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host
PT cells transfected or transfected with DNA encoding a human SCF.
XX
PS Example 3; SEQ ID NO 32; 210pp; English.

CC of protein synthesis, in genetic therapy in humans and other mammals, and
CC in developing transgenic mammalian species which may serve as eukaryotic
CC hosts for production of SCF and SCF products in quantity. The SCF is
CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,
CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelocleiosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroidlastic anaemia, Di Guglielmo
CC syndrome, congenitive splenomegaly, Kala awar, sarcoidosis, primary
CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,
CC fulminating septicemia, malaria, vitamin B 12 and folic acid deficiency,
CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
CC disorders such as plebaldism and vitiligo. The SCF are also useful for
CC treating neurological damage, infertility states, intestinal damage
CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
CC for enhancing haematopoietic recovery after acute blood loss and as a
CC boost to the immune system for fighting neoplasia (cancer). The present
CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 859
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX
AC AAQ75707;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PI WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESCO files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAGTAAA 1536
 |||||
 DB 18 TAAAAAAGTAAA 1

RESULT 860

AAQ33789
 ID AAQ33789 standard; DNA; 21 BP.

XX AAQ33789;
 AC
 XX

DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA2.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Boe taurus.
 OS

PN W09213102-A1.

XX 06-AUG-1992.
 PD

XX 15-JAN-1992; 92WO-US000340.
 PF

XX 15-JAN-1991; 91US-00642342.
 PR

XX (GENM-) GENMARK.
 PA

XX Georges M. Massey JM;
 PI

XX WPI; 1992-284684/34.
 DR

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 245; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 545 TGTGTCGTCGTGTCGTG 562
 |||||
 DB 3 TGTGTCGTCGTGTCGTG 20

RESULT 861

AAQ75702/C
 ID AAQ75702 standard; DNA; 21 BP.

XX AAQ75702;
 AC

XX 04-AUG-1995 (first entry)
 DT

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.
 OS

XX JP06303997-A.
 PN

XX 01-NOV-1994.
 PD

XX 16-APR-1993; 93JP-00112515.
 PF

XX 16-APR-1993; 93JP-00112515.
 PR

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA

XX WPI; 1995-018287/03.
 DR

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAGTAAA 1536
 |||||
 DB 18 TAAAAAAGTAAA 1

RESULT 862

AAQ75671/C
 ID AAQ75671 standard; DNA; 21 BP.

XX AAQ75671;
 AC

XX 04-AUG-1995 (first entry)
 DT

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.
 OS

XX JP06303997-A.
 PN

XX 01-NOV-1994.
 PD

XX 16-APR-1993; 93JP-00112515.
 PF

XX 16-APR-1993; 93JP-00112515.
 PR

```

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match          1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1519 TAAAAAAAAAAAGTAAA 1536
      |||||
Db      18 TAAAAAAAAAAAAAAAAA 1

RESULT 863
AAQ75675/c
ID AAQ75675 standard; DNA; 21 BP.
XX
XX AAQ75675;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

```

```

Query Match          1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1519 TAAAAAAAAAAAGTAAA 1536
      |||||
Db      18 TAAAAAAAAAAAAAAAAA 1

RESULT 864
AAQ75674/c
ID AAQ75674 standard; DNA; 21 BP.
XX
XX AAQ75674;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1519 TAAAAAAAAAAAGTAAA 1536
      |||||
Db      18 TAAAAAAAAAAAAAAAAA 1

RESULT 865
AAQ75687/c
ID AAQ75687 standard; DNA; 21 BP.
XX
XX AAQ75687;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

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```
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAGTAAA 1536
Db |||||||||
18 TAAAAAAAAGTAAA 1
XX
XX RESULT 866
XX AAQ75718/c
XX ID AAQ75718 standard; DNA; 21 BP.
XX AC AAQ75718;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

```
CC CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC CC and using the aggregate of mRNAs as the template for each reverse
CC CC transcription primer; (b) digesting each of the prepared aggregates of
CC CC the double-stranded cDNAs with restriction enzyme and; (c)
CC CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAGTAAA 1536
Db |||||||||
18 TAAAAAAAAGTAAA 1
XX
XX RESULT 867
XX AAQ75690/c
XX ID AAQ75690 standard; DNA; 21 BP.
XX AC AAQ75690;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAGTAAA 1536
Db |||||||||
18 TAAAAAAAAGTAAA 1
XX
XX RESULT 868
XX AAQ75678/c
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ID AAQ75678 standard; DNA; 21 BP.
XX
XX AAQ75678;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1519 TAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 869
AAQ75688/c
ID AAQ75688 standard; DNA; 21 BP.
XX
XX AAQ75688;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1519 TAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 870
AAQ75715/c
ID AAQ75715 standard; DNA; 21 BP.
XX
XX AAQ75715;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

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CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 874
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX
AC AAQ75705;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 875
AAQ75672/c
ID AAQ75672 standard; DNA; 21 BP.
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XX
XX AAQ75672;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 876
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX
AC AAQ75706;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1519 TAAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 877
AAQ75685/c
ID AAQ75685 standard; DNA; 21 BP.
AC
XX AAQ75685;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP6303997-A.
PN
XX 16-APR-1993; 93JP-00112515.
PD
XX 01-NOV-1994.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1519 TAAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1519 TAAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 878
AAQ75699/c
ID AAQ75699 standard; DNA; 21 BP.
AC
XX AAQ75699;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP6303997-A.
PN
XX 16-APR-1993; 93JP-00112515.
PD
XX 01-NOV-1994.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1519 TAAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 879
AAQ75704/c
ID AAQ75704 standard; DNA; 21 BP.
AC
XX AAQ75704;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
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XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAAGTAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
RESULT 880
AAQ75708/C
ID AAQ75708 standard; DNA; 21 BP.
XX
AC AAQ75708;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP06303997-A.
PN
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
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CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAAGTAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
RESULT 881
AAQ75717/C
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP06303997-A.
PN
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAAGTAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
RESULT 882
AAQ75673/C
ID AAQ75673 standard; DNA; 21 BP.
XX
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AC	AAQ75673;
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DT	04-AUG-1995 (first entry)
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KM	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	
PF	16-APR-1993; 93JP-00112515.
PP	
PR	16-APR-1993; 93JP-00112515.
XX	
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
DR	WI; 1995-018287/03.
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
PT	by digestion with restriction enzymes.
XX	
PS	Disclosure; Page 7; 11pp; Japanese.
CC	
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENBSEQ files AAQ7567-07578)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
XX	
SO	Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
QY	
DB	Query Match 1.1%; Score 14.8; DB 1; Length 21; Best Local Similarity 88.9%; Pred. No. 4.2e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0 1519 TAAAAAAAAAAAAAGTAAA 1536 18 TAAAAAAAAAAAAAAAAA 1
RESULT 883	
AAQ75677/C	
ID	AAQ75677 standard; DNA; 21 BP.
XX	
AC	AAQ75677;
XX	
DT	04-AUG-1995 (first entry)
XX	
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KM	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	
PF	16-APR-1993; 93JP-00112515.
PP	
PR	16-APR-1993; 93JP-00112515.
XX	
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	

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DR      WP1; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
XX
XX      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      1.1%; Score 14.8; DB 1; Length 21;
XX      Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAAAAAAGTAAA 1536
DB      18 TAAAAAAAAAAAAAAAAA 1
XX
XX      RESULT 884
XX      AAQ75683/c
XX      ID      AAQ75683 standard; DNA; 21 BP.
XX
XX      AAQ75683;
XX      AC
XX      DT      04-AUG-1995 (first entry)
XX
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
XX      aggregate; restriction enzyme; 88.
XX
XX      Synthetic.
XX      OS
XX      JF06303997-A.
XX      PN
XX      01-NOV-1994.
XX      PD
XX      16-APR-1993; 93JP-00112515.
XX      PE
XX      16-APR-1993; 93JP-00112515.
XX      PR
XX      16-APR-1993; 93JP-00112515.
XX      PA
XX      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX      DR
XX      WP1; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
XX
XX      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      1.1%; Score 14.8; DB 1; Length 21;
XX      Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



```

OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 885
AAQ75710/C
ID AAQ75710 standard; DNA; 21 BP.
XX
XX AAQ75710;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
OS
XX Synthetic.

OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 886
AAQ75701/C
ID AAQ75701 standard; DNA; 21 BP.
XX
XX AAQ75701;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
OS
XX Synthetic.

```

```

PN      JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ      Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 887
AAQ75709/C
ID AAQ75709 standard; DNA; 21 BP.
XX
XX AAQ75709;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
OS
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ      Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

CC transcripction primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electroporating the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 888
AAQ0391 ID AAQ0391 standard; DNA; 21 BP.
XX
AC AAQ0391;
XX
DT 08-JAN-1996 (first entry)
XX
DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
KW CP-1; HLA; dqa; 3' ribonucleoside; self-addressable electronic device;
KM SMD; hybridisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 21 /*tag= a
FT /note= "3' ribonucleoside terminal"
XX
PN WO9512808-A1.
XX
PD 11-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012270.
XX
PR 01-NOV-1993; 93US-00146504.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E;
XX
DR WPI; 1995-185870/24.
XX
PT New self-addressable electronic devices - used for multi-step and
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT and bio:polymer synthesis.
XX
PS Example 1; Page 40; 86pp; English.
XX
CC The sequences represented by, AAQ0390-90401 are synthetic DNA probes
CC containing 3' ribonucleoside terminl. The sequences shown in AAQ0402-15
CC are synthetic DNA probes with 5' amino terminl. These sequences were
CC specific for the polymorphisms of HLA gene dqa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SMD) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 TAAAAAAAAAAGTAAA 1537
Db 18 TAAAAAAAAAAAAAAAAA 18
RESULT 890
AAV35395 ID AAV35395 standard; DNA; 21 BP.
XX

QY 1520 TAAAAAAAAAAGTAAA 1537
Db 18 TAAAAAAAAAAAAAAAAA 18
RESULT 889
AA110743 ID AA110743 standard; RNA; 21 BP.
XX
AC AA110743;
XX
DT 09-SEP-1996 (first entry)
XX
DE Oligonucleotide probe, CP-1.
XX
KW Electronically self-addressable device; ED; electrode; current source;
KM attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 21 /*tag= a
FT /note= "3'-ribonucleoside terminus"
XX
PN WO9601836-A1.
XX
PD 25-JAN-1996.
XX
PF 05-JUL-1995; 95WO-US008570.
XX
PR 07-JUL-1994; 94US-00271882.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
DR WPI; 1996-097582/10.
XX
PF Electronically self-addressable device - used for electronic control of,
PT e.g. nucleic acid hybridisation.
XX
PS Example 1; Page 60; 155pp; English.
XX
CC The sequences given in AA110742-67 are synthetic oligonucleotides which
CC are used in the construction of the electronically self-addressable
CC device (ED) of the invention. The ED comprises a substrate, an electrode
CC or opt. a number of electrodes supported by the substrate, a current
CC source operatively connected to the electrode and an attachment layer
CC adjacent to the electrode which is permeable to a counterion but not
CC permeable to a molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 TAAAAAAAAAAGTAAA 1537
Db 18 TAAAAAAAAAAAAAAAAA 18
RESULT 890
AAV35395 ID AAV35395 standard; DNA; 21 BP.
XX

```
AC AAV35395;
XX
XX 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #8.
XX
XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
XX vaccines; infection; protection; primer; ss.
XX
XX Synthetic.
XX
XX MO9822596-A1.
XX
XX 28-MAY-1998.
XX
XX 19-NOV-1997; 97WO-JP004216.
XX
XX 19-NOV-1996; 96JP-00323412.
XX
XX (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX (JAPG) NIPPON ZEON KK.
XX
XX Kojima A, Kurata T, Yasuda A;
XX
XX WPI; 1998-312481/27.
XX
XX Recombinant vaccinia virus containing fusion H1B gag gene - for
XX production in host cells of gag protein for use as vaccine.
XX
XX Example 1; Page 66; 84pp; Japanese.
XX
XX AAV35388-V35414 are primers used in a method which results in a
XX recombinant vaccinia virus comprising of a gag gene from a retrovirus
XX such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
XX region (30-300 bases in length) of a retroviral gene other than the gag
XX gene. The gag gene may be altered so as to produce a gag protein modified
XX from the natural sequence by the addition, deletion or substitution of at
XX least 1 amino acid residue. The fusion gene is inserted into a region of
XX a vaccinia virus not essential to its propagation, to give a recombinant
XX vaccinia virus vector which is used to transform a host cell (such as
XX HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
XX culturing the host cell produces particulate structures containing the
XX fusion gag protein. The recombinant vaccinia virus or the fusion gag
XX protein particles may be used in the production of vaccines for
XX protecting against infection with retroviruses such as HIV
XX
XX
XX Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred.No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX Db 3 AAAAAAAAAAAAAAAAAA 20
XX
XX
XX RESULT 891
XX AA226403
XX ID AA226403 standard; DNA; 21 BP.
XX
XX AA226403;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 592.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
```

```
XX
XX Homo sapiens.
XX
XX OS
XX MO9841648-A2.
XX
XX PN
XX
XX 24-SEP-1998.
XX
XX PD
XX
XX 19-MAR-1998; 98WO-US005419.
XX
XX PF
XX
XX 20-MAR-1997; 97US-0041057P.
XX
XX PR
XX
XX (VART-) VARIAGENICS INC.
XX
XX PA
XX
XX Housman D, Ledley FD, Stanton VP;
XX
XX PI
XX
XX WPI; 1998-521232/44.
XX
XX DR
XX
XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX PT
XX
XX PS Disclosure; Fig 7; 605pp; English.
XX
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX CC graft versus host disease. The method can also be used to remove
XX CC malignant cells from bone marrow transplants. AA25812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX
XX Sequence 21 BP; 12 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX QY 1514 TTAATTAAAAA 1531
XX |||||
XX Db 4 TTTTAAAAA 21
XX
XX
XX RESULT 892
XX AA226226
XX ID AA226226 standard; DNA; 21 BP.
XX
XX AA226226;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 415.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX OS Homo sapiens.
XX
XX PN MO9841648-A2.
XX
```

```

XX 24-SEP-1998.
PD 19-MAR-1998; 98WO-US005419.
XX 19-MAR-1998; 98WO-US005419.
XX 20-MAR-1997; 97US-0041057P.
XX (VARI-) VARIAGENICS INC.
XX Houseman D, Ledley PD, Stanton VP;
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumors, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AA225812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 2 A; 6 C; 12 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 422 GAGTGGCGGCTGCGCGCC 439
XX ||| ||||| |||||
XX 3 GAGGCGCGCGCGCGCGCC 20
XX
XX RESULT 893
XX AAX81302
XX ID AAX81302 standard; DNA; 21 BP.
XX
XX AAX81302;
XX
XX 20-AUG-1999 (first entry)
XX
XX 3' ribonucleoside oligonucleotide probe CP-1.
XX
XX Microelectronic device; multi-step reaction; microscopic format;
XX ion-permeable permeation layer; electrode; electrical control; transport;
XX attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT mlec_RNA 21
XX FT /*tag= a
XX
XX W09929711-A1.
XX
XX 17-JUN-1999.
XX

```

```

PF 01-DEC-1998; 98WO-US025475.
XX
XX 05-DEC-1997; 97US-00986065.
XX
XX (NANO-) NANOGEN INC.
XX
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
XX
XX Example 1; Page 89; 179pp; English.
XX
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this invention is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific binding
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence represents a probe used to exemplify the invention
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAA 1537
XX ||| ||||| |||||
XX 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 894
XX AAV71751/C
XX ID AAV71751 standard; DNA; 21 BP.
XX
XX AAV71751;
XX
XX 15-MAR-1999 (first entry)
XX
XX Human V3 loop HIV receptor p30/PHAP1 sense PCR primer.
XX
XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
XX p30 protein; PHAP1; infection; therapy; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX W09840480-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-EP001409.
XX
XX 12-MAR-1997; 97US-0040969P.
XX
XX (INSP ) INST PASTEUR.
XX (CNRS ) CENT NAT RECH SCI.
XX

```

[illegible]

PS Disclosure; Page 62; 195pp; English.

CC The invention identifies a genetic locus ASTH1, associated with asthma,
CC mapped to human chromosome 11p. ASTH1 and ASTHJ are genes present
CC within the locus, located close to each other on human chromosome 11p.
CC and have similar patterns of expression, and common sequence motifs. The
CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions
CC and anti-ASTH1 antibodies are useful in the identification of individuals
CC predisposed to development of asthma, and for the modulation of gene
CC activity in vivo for prophylactic and therapeutic purposes. The ASTH1
CC protein is useful as an immunogen to raise specific antibodies, in drug
CC screening for compositions that mimic or modulate ASTH1 activity or
CC expression, including altered forms of ASTH1 protein, and as a
CC therapeutic. Sequences AA218366-218509 represent polymorphisms in the
CC ASTH1 and ASTHJ genes

XX XX Sequence 21 BP; 0 A; 9 C; 1 G; 10 T; 0 U; 1 Other;

SQ Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1225 CTCCTAGCTTACGTTTCCTC 1244
||| ||| ||| ||| ||| |||
Db 1 CTCCTTCTCTGTGCCTTCCTC 20

RESULT 896
AAAX26973/c
ID AAX26973 standard; cDNA; 21 BP.
XX
AC AAX26973;
XX
DT 25-JUN-1999 (first entry)
XX
DE Primer used to reverse transcribe mammaglobin RNA.
XX
KW Human; mammary-specific protein; mammaglobin; antigen; vaccine;
KW mammaglobin-expressing cancer; breast cancer;
KM autologous tumor lymphocyte; diagnosis; marker; primer; ss.
XX
OS Synthetic.
XX
PN WO9914230-A1.
PD
XX 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US017991.
XX
PR 18-SEP-1997; 97US-00933149.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Watson MA, Fleming TP;
DR WPI; 1999-244021/20.
XX
XX Mammaglobin, secreted protein overexpressed in breast cancer.

PS Example 2; Page 55; 60pp; English.

CC The present primer was used to reverse transcribe RNA encoding a human
CC mammary-specific protein, designated mammaglobin. The specification
CC describes a process comprising a mammaglobin antigen that is recognized
CC by B and/or Tc cells specific for the natural, secreted and glycosylated
CC form of mammaglobin polypeptide. This protein, or recombinant vectors
CC that express it, are used in vaccines for treating mammaglobin-
CC expressing cancers, specifically of the breast. Such cancers can also be
CC treated using autologous tumor lymphocytes activated ex vivo with an
CC mammaglobin antigen, then returned to the patient. Expression of
CC mammaglobin is elevated in 27% of stage I primary breast cancers, so it
XX represents a marker useful for diagnosis of this disease

```

SQ Sequence 21 BP, 0 A, 0 C, 0 G, 21 T, 0 U, 0 Other;
DE Query Match 1.1%; Score 14.8; DB 1; Length 21;
DE Best Local Similarity 88.9%; Pred. No. 4.2e+02;
DE Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
DB 21 AAAAAAAAAAAAAA 4

RESULT 897
AAZ44350/C
ID AAZ44350 standard; DNA; 21 BP.
XX
AC AAZ44350;
XX
DT 04-APR-2000 (first entry)
XX
DE Protein kinase inhibiting primer #12.
XX
KM Antimicrobial; cytostatic; immunosuppressive; protein kinase;
KM prophylactic; therapy; treatment; cancer; autoimmune disease;
KM pathogenic microorganism; primer; ss.
XX
OS Unidentified.
XX
PN US5998596-A.
XX
PD 07-DEC-1999.
XX
PF 04-APR-1995; 95US-00416214.
XX
PR 04-APR-1995; 95US-00416214.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Bergan R, Neckers L;
XX
WPI; 2000-104623/09.
XX
Oligonucleotides inhibiting protein kinase, useful for treating diseases
PT such as cancer and autoimmune disease.
XX
PS Example 6; Col 27-28; 26pp; English.
XX
CC This invention describes novel purified aptameric oligonucleotides which
CC have antimicrobial, cytostatic and immunosuppressive activity. The
CC oligonucleotides are useful for binding to and preventing or inhibiting
CC the biological function of a protein kinase or a target molecule and for
CC detecting the presence or absence of a target molecule in biological
CC samples. The oligonucleotides are also useful for prophylactic and
CC therapeutic treatment of diseases such as cancer, autoimmune diseases and
CC diseases caused by pathogenic microorganisms. This sequence represents a
CC primer used in the method of the invention
XX
SQ Sequence 21 BP, 0 A, 0 C, 0 G, 21 T, 0 U, 0 Other;
DE Query Match 1.1%; Score 14.8; DB 1; Length 21;
DE Best Local Similarity 88.9%; Pred. No. 4.2e+02;
DE Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
DB 21 AAAAAAAAAAAAAA 4

RESULT 898
AAA80318
ID AAA80318 standard; DNA; 21 BP.
XX
AC AAA80318;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human ASTH1J 5' region polymorphic site, SEQ ID NO:66.
XX
KM ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KM bronchial hyperreactivity; ets family; transcription factor;
KM splice variant; genetic predisposition; polymorphism; antibody;
KM drug screening; prophylaxis; therapy; diagnosis;
KM single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
PN US6087485-A.
XX
PD 11-JUL-2000.
XX
PF 21-JAN-1998; 98US-00009913.
XX
PR 21-JAN-1997; 97US-0035663P.
XX
PR 01-JUL-1997; 97US-0051432P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, North M, Cardon L, Buckler A;
PI Brooks-Wilson AR, Carey AH;
XX
WPI; 2000-505109/45.
XX
XX New nucleic acids other than naturally occurring chromosomes encoding
PT ASTH1 protein, for e.g., screening compositions that modulate expression
PT or function of ASTH1 proteins or as diagnostics for genetic
PT predisposition to asthma.
XX
PS Example; Col 41-42; 131pp; English.
XX
CC The invention relates to the ASTH1 locus on the short arm of human
CC chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC are associated with a genetic predisposition to asthma and bronchial
CC hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC directions with the ASTH1 locus, and have similar patterns of expression
CC and common sequence motifs. They are both expressed in trachea, lung and
CC several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC family of transcription factors, which have been implicated in the
CC activation of a variety of genes including the TCRA gene and cytokine
CC genes known to be important in the aetiology of asthma. Both ASTH1I and
CC ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC transcripts has no effect on the open reading frame of ASTH1J, as the
CC exons involved are all 5' to the start codon in exon b. In contrast,
CC alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC isoforms. The invention also encompasses mouse asth1 protein. The ASTH1
CC nucleic acids are useful as diagnostics to identify a hereditary
CC predisposition to asthma, as probes for identifying ASTH1 related genes,
CC for identifying expression of the gene in a biological specimen, and for
CC generating genetically modified non-human animals or site specific gene
CC modifications in cell lines. The encoded ASTH1 proteins are useful as
CC immunogens to raise specific antibodies; in drug screening for
CC compositions that mimic or modulate activity or expression of ASTH1I
CC and/or ASTH1J (including altered forms of these proteins); and as a
CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC antibodies are useful in the identification of individuals predisposed to
CC development of asthma, and for modulation of gene activity in vivo for
CC prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC proteins or active fragments thereof may be used to modulate or reduce
CC bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ Sequence 21 BP, 0 A, 9 C, 1 G, 10 T, 0 U, 1 Other;
DE Query Match 1.1%; Score 14.8; DB 1; Length 21;
DE Best Local Similarity 80.0%; Pred. No. 4.2e+02;
DE Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      1225 CTCTAGCTTCTAGCTTCCTC 1244
      |||||:|||||
Db      1  CTCTTCTCTCTCTCTCTCCTC 20

RESULT 899
AAAF9707/c
ID      AAf9707 standard; DNA; 21 BP.
AC      AAf9707;
XX
XX      12-JUN-2001 (first entry)
XX
XX      Immunostimulatory nucleic acid #823.
XX
XX      Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX      immunostimulatory; tumour; viral infection; bacterial infection;
XX      fungal infection; parasitic infection; cancer; asthma;
XX      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX      Synthetic.
XX
XX      WO200122972-A2.
XX
XX      05-APR-2001.
XX
XX      25-SEP-2000; 2000WO-US026383.
XX
XX      25-SEP-1999; 99US-0156113P.
XX      27-SEP-1999; 99US-0156135P.
XX      23-AUG-2000; 2000US-0227436P.
XX
XX      (IOWA ) UNIV IOWA RES FOUND.
XX      (COLE-) COLEY PHARM GMBH.
XX
XX      Krieg AM, Schetter C, Vollmer J;
XX
XX      WPI; 2001-273485/28.
XX
XX      Vaccinating against tumor, infectious diseases, allergies and asthma
XX      using immunostimulatory Py-rich and TG nucleic acids.
XX
XX      Claim 101; Page 56; 338pp; English.
XX
XX      The present invention relates to a method for stimulating an immune
XX      response. The method comprises administering an immunostimulatory nucleic
XX      acid to a non-rodent subject in sufficient quantity to stimulate an
XX      immune response. The present sequence is one such immunostimulatory
XX      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX      haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX      streptococcus), fungal antigens and/or parasitic antigens. The method is
XX      also useful for preventing cancer, asthma, infectious disease, allergy or
XX      immune deficiency. The present sequence can also be used to redirect a
XX      Th1 to a Th1 immune response and to activate immune cells. Note: the
XX      present sequence may have a phosphorothioate backbone
XX
XX      Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAAGTAAAA 1537
      |||||:|||||
Db      21  AAAAAAAAAAAAAAAAAAAAA 4

RESULT 900
AAH42480/c
ID      AAH42480 standard; DNA; 21 BP.

```

```

XX      AAH42480;
XX
XX      01-OCT-2001 (first entry)
XX
XX      Oligonucleotide used to produce branched chain compounds.
XX
XX      Branched chain compound; nucleic acid synthesis; primer extension;
XX      reverse transcription; nucleic acid hybridization;
XX      nucleic acid amplification; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1
XX      FT      /*tag= a
XX      FT      /note= "NH2-C6 attached"
XX      modified_base 4
XX      FT      /*tag= b
XX      FT      /note= "NH2-C6 attached"
XX      FT      5..7
XX      FT      /*tag= c
XX      FT      /note= "branch present"
XX
XX      EP111068-A1.
XX
XX      27-JUN-2001.
XX
XX      21-DEC-1999; 99EP-00125484.
XX
XX      21-DEC-1999; 99EP-00125484.
XX
XX      (LION-) LION BIOSCIENCE AG.
XX      (VBCG-) VBC GENOMICS GMBH.
XX
XX      Schmidt W, Hiller R, Huber M, Mueller M;
XX
XX      WPI; 2001-466959/51.
XX
XX      Branched compounds useful in e.g. nucleic acid synthesis reaction
XX      comprises nucleic acid moieties optionally extended by a polymerase.
XX
XX      Example 1; Page 10; 31pp; English.
XX
XX      The specification describes branched compounds containing nucleic acid
XX      moieties optionally extended by a polymerase. The branched chain
XX      compounds of the invention are used in nucleic acid synthesis reaction,
XX      primer extension reaction, reverse transcription reaction of RNA into
XX      cDNA, nucleic acid hybridization experiment (for identifying sequence of a
XX      nucleic acid), and nucleic acid amplification experiment (for analysing
XX      the expression pattern of genes). The compounds are also used in solid-
XX      phase enzymatic reactions. The present sequence was used in the course of
XX      the invention to produce branched chain compounds
XX
XX      Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAAGTAAAA 1537
      |||||:|||||
Db      21  AAAAAAAAAAAAAAAAAAAAA 4

RESULT 901
ABS78428/c
ID      ABS78428 standard; DNA; 21 BP.
AC      ABS78428;
XX
XX      13-DEC-2002 (first entry)
XX

```


DE Angiogenesis inhibitory oligonucleotide #912.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KM rubosis; Osler-Weber Syndrome; myocardial angiogenesis;
KM plaque neovascularisation; telangiectasia; haemophilic joint;
KM angiodioma; wound granulation; intestinal adhesion; atherosclerosis;
KM scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
XX 11-JUN-2002.
PD
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
PI
XX MPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 35; 276pp; English.
PS
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC including a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAATAAAA 1537
DB 21 AAAAAAAAAAATAAAA 4
XX
RESULT 902
ABL39404/C
ID ABL39404 standard; DNA; 21 BP.
XX
AC ABL39404;
XX
XX 16-APR-2002 (first entry)
DT
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 840.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20.
KM angio genesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1: 21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
XX 27-DEC-2001.
PD
XX 22-JUN-2001; 2001WO-US020154.
XX
XX 22-JUN-2000; 2000US-0213346P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G;
PI
XX MPI; 2002-154611/20.
XX
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 309; 312pp; English.
PS
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAATAAAA 1537
DB 21 AAAAAAAAAAATAAAA 4
XX
RESULT 903
ABS97830/C
ID ABS97830 standard; DNA; 21 BP.
XX
AC ABS97830;
XX
XX 23-DEC-2002 (first entry)
DT
XX
DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.
XX
XX Human; de; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KM cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSB;
KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMNT;
KM NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX

KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KM multidrug resistance associated protein 3; cancer; prostate;
KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR4; CHMR5;
KM altered drug metabolism; cardiovascular function; colorectal tumour;
KM central nervous system; pulmonary; immunological; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN M0200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
PS WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
XX Example 16; Page 130; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome p450 A1 (CYP450A1), cytochrome p450 A2 (CYP450A2),
CC cytochrome p450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC inhibitor (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 545 TGTGGTGGCTGTGGCTGG 562
DB 19 TGTGTGTGCTGTGTGTG 2
RESULT 904
AAD51323/c
ID AAD51323 standard; DNA; 21 BP.
XX
AC AAD51323;
XX
DT 16-APR-2003 (first entry)
XX
DE Regular oligo dt primer used to illustrate the method of the invention.
XX
KM Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KM gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KM musculoskeletal damage; ss.
XX
OS Unidentified.
XX
PN M0200290579-A1.
XX
PD 14-NOV-2002.
XX
PF 03-MAY-2002; 2002WO-AU000553.
XX
PR 04-MAY-2001; 2001AU-00004809.
XX
PR 29-JUN-2001; 2001US-00896941.
XX
PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
PI Brandon RB;
XX
PS WPI; 2003-120558/11.
XX
PT Assessing condition e.g. athletic ability, stage of disease, presence of
PT drugs, response to exercise, response to vaccines, therapies, nutritional
PT states, of performance animal involves analyzing nucleic acid expression.
XX
XX Disclosure; Page 46; 87pp; English.
XX
PS The invention relates to a method for assessing a condition of a
PS performance animal. The method involves determining in sample abundance
PS of expressed target nucleic acid; transmitting digital sample signal to
PS remote diagnostic server; processing digital sample signal at remotely
PS located database to correlate digital signal with digital information and
PS returning report of particular condition of animal. The method is useful
PS for assessing a condition of a performance animal preferably human, dog
PS or camel. The condition can be an athletic ability and a condition that
PS enhances, hinders, impedes or does not change an expected ability of the
PS performance animal; and also normal, pre-clinical, overt progress and/or
PS stage of disease, undiagnosed or unclassified conditions, presence of
PS drugs, response to exercise, response to vaccines, therapies, nutritional
PS states and response to environmental conditions. Diseases assessed by the
PS invention include laminitis, lameness, viral or bacterial disease,
PS gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
PS musculoskeletal damage or disorders and joint diseases. The present
PS sequence is a primer used to illustrate the method of the invention
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4

```
RESULT 905
ACH03246/C
ID ACH03246 standard; DNA; 21 BP.
XX
AC ACH03246;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #881.
XX
KM Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KM antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KM psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KM inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PE 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Kriegl AM, Berg DJ;
XX
DR MPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 33; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAGTAAAA 4
RESULT 906
ADB37209/C
ID ADB37209 standard; DNA; 21 BP.
XX
AC ADB37209;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #823.
XX
KM db; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KM hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
```

```
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PERE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR MPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAGTAAAA 4
RESULT 907
ADK01309/C
ID ADK01309 standard; DNA; 21 BP.
XX
AC ADK01309;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #29.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR MPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
```

XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acids in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

SO Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
|||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 908
ADK01318/c
ID ADK01318 standard; DNA; 21 BP.

AC ADK01318;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #38.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

PN 04-SEP-2003.

PD 28-FEB-2002; 2002DE-01008794.

PF 28-FEB-2002; 2002DE-01008794.

PR (DEGS) DEGUSA BIOACTIVES GMBH.

PA Boekenkamp D, Dieck HT, Hoppe H;

PI WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid; useful for analyzing expression

PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acids in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

SO Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
|||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 909
ADK01323/c
ID ADK01323 standard; DNA; 21 BP.

AC ADK01323;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #43.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

PN 04-SEP-2003.

PD 28-FEB-2002; 2002DE-01008794.

PF 28-FEB-2002; 2002DE-01008794.

PR (DEGS) DEGUSA BIOACTIVES GMBH.

PA Boekenkamp D, Dieck HT, Hoppe H;

```

XX DR WPI; 2003-714082/68.
XX
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX
XX PS Example; Page 5; 8pp; German.
XX
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX
XX SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAAGTAAAA 1537
XX DB 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 910
XX ID ADK01344/C
XX AC ADK01344;
XX ADK01344;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #64.
XX
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.

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XX XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PA
XX BX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX DR WPI; 2003-714082/68.
XX
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX
XX PS Example; Page 6; 8pp; German.
XX
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAAGTAAAA 1537
XX DB 21 AAAAAAAAAAAAAAAAAA 4
XX
XX RESULT 911
XX ID ADK01340/C
XX AC ADK01340;
XX ADK01340;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #60.
XX
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.

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XX 28-FEB-2002; 2002DE-01008794.
PF
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
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CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 912
ADK01319/c
ID ADK01319 standard; DNA; 21 BP.
XX
AC ADK01319;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #39.
XX
KM seq, hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
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XX DE10208794-A1.
PN
XX
PD 04-SEP-2003.
PD
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
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CC conducting properties and especially in the form of a chip. Its surface
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CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
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CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 913
ADK01328/c
ID ADK01328 standard; DNA; 21 BP.
XX
AC ADK01328;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #48.
XX
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XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX Rattus sp.
XX DE10208794-A1.
XX 04-SEP-2003.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX (DEGS) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX Example; Page 5; 8pp; German.
XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
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CC least once in each nucleic acid and a 3'-variable, discriminatory region
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CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
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CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
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CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 914
ADK01335/C
ID ADK01335 standard; DNA; 21 BP.
XX AC
XX ADK01335;
XX

DT 06-MAY-2004 (first entry)
XX Rat DNA microarray capture oligonucleotide #55.
DE
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX Rattus sp.
XX DE10208794-A1.
XX 04-SEP-2003.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX (DEGS) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX Example; Page 6; 8pp; German.
XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
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CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
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CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
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CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
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CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2
RESULT 915
ADK01302/C


```
ID ADK01302 standard; DNA; 21 BP.
XX
XX AC ADK01302;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #22.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGUS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8bp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
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CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SO Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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RESULT 916
ADK01317/c
ID ADK01317 standard; DNA; 21 BP.
XX
XX AC ADK01317;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #37.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGUS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8bp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SO Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

Oy      1520 AAAAAAAAAAGTAAA 1537
      ||||| ||||| |||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 917
ADK01334/C
ID      ADK01334 standard; DNA; 21 BP.
XX
AC      ADK01334;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Rat DNA microarray capture oligonucleotide #54.
XX
KW      ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW      blood; nerve; germ cell; food additive; food supplement.
XX
OS      Rattus sp.
XX
PN      DE10208794-A1.
XX
PD      04-SEP-2003.
XX
PF      28-FEB-2002; 2002DE-01008794.
XX
PR      28-FEB-2002; 2002DE-01008794.
XX
PA      (DEGSA ) DEGUSSA BIOACTIVES GMBH.
XX
PI      Boekenkamp D, Dieck HT, Hoppe H;
XX
DR      WPI; 2003-714082/68.
XX
PT      Sorting single-stranded nucleic acid, useful for analyzing expression
PT      patterns and screening active agents, uses capture agent with variable
PT      and constant regions.
XX
PS      Example; Page 5; 8pp; German.
XX
CC      This invention describes a novel method for sorting single-stranded
CC      nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC      reading out, where the nucleic acids are selectively bound using capture
CC      agents that are (a) immobilised on the surface of a solid matrix and (b)
CC      comprise variable and non-variable regions. The capture oligonucleotides
CC      have a 5'-invariable anchor region, the complement of which is present at
CC      least once in each nucleic acid and a 3'-variable, discriminatory region
CC      that comprises all possible combinations of up to 10 nucleotides to allow
CC      binding of particular sorts of single stranded nucleic acids. The capture
CC      agents are particularly locked nucleic acids (LNA) and the anchor region
CC      comprises a sequence of 10-50, particularly 15-25, T residues. The
CC      capture oligonucleotides are biotinylated and immobilised on a surface by
CC      interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC      metal, resin, gel, crystalline material and/or membrane, having semi-
CC      conducting properties and especially in the form of a chip. Its surface
CC      is particularly a layer of (bio)molecular filaments and binding of single
CC      stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC      physical, stimulated by an electrical field or through a molecular sieve.
CC      The method is used (i) for analysis of patterns, especially in mucosal,
CC      hair root, blood, nerve or germ cells and (ii) for determining the
CC      activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC      additives or supplements, especially minerals, trace elements, organic
CC      acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC      mixtures. The method provides rapid, inexpensive and reproducible
CC      representation of differences in pools of nucleic acids from cells. It
CC      allows imaging of the complete pattern of all nucleic acids in a cell, and
CC      can detect very small differences in the nucleic acid pool. Since the
CC      method is based on comparison of nucleic acid pools, not individual
CC      genes, matrix mislabelisation is possible. ADK01281-ADK01344 represent
CC      capture probes used in the method of the invention.
XX
Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

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Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1520 AAAAAAAAAAGTAAA 1537
      ||||| ||||| |||||
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 918
ADK01303/C
ID      ADK01303 standard; DNA; 21 BP.
XX
AC      ADK01303;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Rat DNA microarray capture oligonucleotide #23.
XX
KW      ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW      blood; nerve; germ cell; food additive; food supplement.
XX
OS      Rattus sp.
XX
PN      DE10208794-A1.
XX
PD      04-SEP-2003.
XX
PF      28-FEB-2002; 2002DE-01008794.
XX
PR      28-FEB-2002; 2002DE-01008794.
XX
PA      (DEGSA ) DEGUSSA BIOACTIVES GMBH.
XX
PI      Boekenkamp D, Dieck HT, Hoppe H;
XX
DR      WPI; 2003-714082/68.
XX
PT      Sorting single-stranded nucleic acid, useful for analyzing expression
PT      patterns and screening active agents, uses capture agent with variable
PT      and constant regions.
XX
PS      Example; Page 5; 8pp; German.
XX
CC      This invention describes a novel method for sorting single-stranded
CC      nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC      reading out, where the nucleic acids are selectively bound using capture
CC      agents that are (a) immobilised on the surface of a solid matrix and (b)
CC      comprise variable and non-variable regions. The capture oligonucleotides
CC      have a 5'-invariable anchor region, the complement of which is present at
CC      least once in each nucleic acid and a 3'-variable, discriminatory region
CC      that comprises all possible combinations of up to 10 nucleotides to allow
CC      binding of particular sorts of single stranded nucleic acids. The capture
CC      agents are particularly locked nucleic acids (LNA) and the anchor region
CC      comprises a sequence of 10-50, particularly 15-25, T residues. The
CC      capture oligonucleotides are biotinylated and immobilised on a surface by
CC      interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC      metal, resin, gel, crystalline material and/or membrane, having semi-
CC      conducting properties and especially in the form of a chip. Its surface
CC      is particularly a layer of (bio)molecular filaments and binding of single
CC      stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC      physical, stimulated by an electrical field or through a molecular sieve.
CC      The method is used (i) for analysis of patterns, especially in mucosal,
CC      hair root, blood, nerve or germ cells and (ii) for determining the
CC      activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC      additives or supplements, especially minerals, trace elements, organic
CC      acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC      mixtures. The method provides rapid, inexpensive and reproducible
CC      representation of differences in pools of nucleic acids from cells. It
CC      allows imaging of the complete pattern of all nucleic acids in a cell, and
CC      can detect very small differences in the nucleic acid pool. Since the
CC      method is based on comparison of nucleic acid pools, not individual

```

CC genes, matrix miniaturisation is possible. ADX01281-ADX01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 919
ADX01327/c
ID ADX01327 standard; DNA; 21 BP.
XX
AC ADX01327;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #47.
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGUS) DEGUSSA BIOACTIVES GMBH.
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; Bpp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible

CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADX01281-ADX01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 920
ADX01338/c
ID ADX01338 standard; DNA; 21 BP.
XX
AC ADX01338;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #58.
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGUS) DEGUSSA BIOACTIVES GMBH.
PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; Bpp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the

CC	stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC	physical, stimulated by an electrical field or through a molecular sieve.
CC	The method is used (i) for analysis of patterns, especially in mucosal,
CC	hair root, blood, nerve or germ cells and (ii) for determining the
CC	activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC	additives or supplements, especially minerals, trace elements, organic
CC	acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC	mixtures). The method provides rapid, inexpensive and reproducible
CC	representation of differences in pools of nucleic acids from cells. It
CC	allows imaging of the complete pattern of all nucleic acid in a cell, and
CC	can detect very small differences in the nucleic acid pool. Since the
CC	method is based on comparison of nucleic acid pools, not individual
CC	genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC	capture probes used in the method of the invention.
XX	
SQ	Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity	86.9%; Pred. No. 4.2e+02;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0
Oy	1520 AAAAAAAAAAGTAAA 1537 Db 18 AAAAAAAAAAAAAAA 1
RESULT 922	
ADK01320/c	
ID	ADK01320 standard; DNA; 21 BP.
XX	
AC	ADK01320;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Rat DNA microarray capture oligonucleotide #40.
XX	
KW	ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM	blood; nerve; germ cell; food additive; food supplement.
XX	
OS	Rattus sp.
XX	
PN	D810208794-A1.
XX	
PD	04-SEP-2003.
XX	
PF	28-FEB-2002; 2002DE-01008794.
XX	
FR	28-FEB-2002; 2002DE-01008794.
XX	
PA	(DEGS) DEGUSSA BIOACTIVES GMBH.
XX	
PI	Boekenkamp D, Dieck HT, Hoppe H;
XX	
WP1	2003-714082/68.
XX	
PT	Sorting single-stranded nucleic acid, useful for analyzing expression
PT	patterns and screening active agents, uses capture agent with variable
XX	and constant regions.
XX	
PS	Example; Page 5; Bpp; German.
XX	
CC	This invention describes a novel method for sorting single-stranded
CC	nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC	reading out, where the nucleic acids are selectively bound using capture
CC	agents that are (a) immobilised on the surface of a solid matrix and (b)
CC	comprise variable and non-variable regions. The capture oligonucleotides
CC	have a 5'-invariable anchor region, the complement of which is present at
CC	least once in each nucleic acid and a 3'-variable, discriminatory region
CC	that comprises all possible combinations of up to 10 nucleotides to allow
CC	binding of particular sorts of single stranded nucleic acids. The capture
CC	agents are particularly locked nucleic acids (LNA) and the anchor region
CC	comprises a sequence of 10-50, particularly 15-25, T residues. The
CC	capture oligonucleotides are biotinylated and immobilised on a surface by

CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 923

ADK01304/c

ID ADK01304 standard; DNA; 21 BP.

AC ADK01304;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #24.

KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KM blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

PS Example; Page 5; Bpp; German.

XX This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at

CC least once in each nucleic acid and a 3'-variable, discriminatory region

CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 924

ADK01306/c

ID ADK01306 standard; DNA; 21 BP.

AC ADK01306;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #25.

KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KM blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

PD 04-SEP-2003.

PF 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

PA (DEGS) DEGUSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

PS Example; Page 5; Bpp; German.

XX This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

SO Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 925
ADK01325/C

ID ADK01325 standard; DNA; 21 BP.

XX AC ADK01325;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #45.

XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGS) DEGUSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

XX Example, Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

SO Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 926
ADK01339/C

ID ADK01339 standard; DNA; 21 BP.

XX AC ADK01339;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #59.

XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGS) DEGUSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

PT and constant regions.
XX
PS Example; Page 6; Bpp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislabelling is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 927
ADK01343/c
ID ADK01343 standard; DNA; 21 BP.
XX
AC ADK01343;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #63.
XX
XX seq; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX

DR WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; Bpp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislabelling is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 928
ADK01301/c
ID ADK01301 standard; DNA; 21 BP.
XX
AC ADK01301;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #21.
XX
XX seq; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX

PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
PS
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
S0 Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 929
ADK01312/c
ID ADK01312 standard; DNA; 21 BP.
XX
XX ADK01312;
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #32.
XX
KM 89; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX

PF 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
PR
XX
XX (DEGS) DEGUSSA BIOACTIVES GMBH.
PA
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
DR
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
PS
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
S0 Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 930
ADK01326/c
ID ADK01326 standard; DNA; 21 BP.
XX
XX ADK01326;
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #46.
XX
KM 89; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX

```
PN DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acids in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX | | | | | | | | | |
XX 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 931
XX ADK01305/c
XX ID ADK01305 standard; DNA; 21 BP.
XX
XX AC ADK01305;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Rat DNA microarray capture oligonucleotide #25.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
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KW blood; nerve; germ cell; food additive; food supplement.
XX
XX Ratus SP.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acids in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAGTAAA 1537
XX | | | | | | | | | |
XX 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 932
XX ADK01310/c
XX ID ADK01310 standard; DNA; 21 BP.
XX
XX AC ADK01310;
XX
XX DT 06-MAY-2004 (first entry)
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```
XX DE Rat DNA microarray capture oligonucleotide #30.
XX
XX 88; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Ractus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acids in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX ||||| |||||
XX 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 933
XX ADK01336/C
XX ID ADK01336 standard; DNA; 21 BP.
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```
XX AC ADK01336;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #56.
XX
XX 88; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Ractus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX
XX Example; Page 6; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acids in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX ||||| |||||
XX 19 AAAAAAAAAAAAAAAAAA 2
XX
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RESULT 934
ADK01342/c
ID ADK01342 standard; DNA; 21 BP.
XX
AC ADK01342;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #62.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
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CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1520 AAAAAAAAAAACTAAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 935
ADK01308/c
ID ADK01308 standard; DNA; 21 BP.
XX
AC ADK01308;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #28.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

```

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 |||||
 18 AAAAAAAAAAAAAAAAA 1

RESULT 936
 ADK01311/c

ID ADK01311 standard; DNA; 21 BP.

AC ADK01311;

XX 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #31.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent

CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

SO Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 |||||
 18 AAAAAAAAAAAAAAAAA 1

RESULT 937
 ADK01321/c

ID ADK01321 standard; DNA; 21 BP.

AC ADK01321;

XX 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #41.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It

```
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislabourisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 938
ADK01322/c
ID ADK01322 standard; DNA; 21 BP.
XX
AC ADK01322;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #42.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
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```
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislabourisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 939
ADK01324/c
ID ADK01324 standard; DNA; 21 BP.
XX
AC ADK01324;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #44.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
```


CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix misattribution is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAAGTAAA 1537
 18 AAAAAAAAAAAAAAAAAA 1

RESULT 940
 ADM96310/C
 ID ADM96310 standard; DNA; 21 BP.
 AC ADM96310;
 XX 17-JUN-2004 (first entry)
 XX Human ATP5F1 gene, RT-PCR primer #1.
 DE Human ATP5F1 gene, RT-PCR primer #1.
 XX ss; human; H+ transporting; mitochondrial ATP synthase; subunit B;
 KW isoform 1; ATP5F1; reverse transcriptase; RT-PCR; primer.
 XX Synthetic.
 OS US2003211483-A1.
 PN 13-NOV-2003.
 PD 09-MAY-2002; 2002US-0014179.
 PE 09-MAY-2002; 2002US-0014179.
 PR 09-MAY-2002; 2002US-0014179.
 XX (SCHR/) SCHROEDER B G.
 PA (CHEN/) CHEN C.
 PA (SCHR/) SCHROTH G P.
 XX Schroeder BG, Chen C, Schroth GP;
 PI WPI; 2003-901581/82.
 DR Entriching low abundance polynucleotides in a sample, useful for gene
 XX expression analysis, comprises exposing the sample to an enzymatically
 PT non-extendable nucleobase oligomer to block polymerase activity on high
 PT abundance species.
 XX Example 1; Page 20; 43pp; English.

The invention relates to a method of enriching a low abundance
 CC polynucleotide in a sample of polynucleotides comprising a low abundance
 CC and a high abundance polynucleotide. The method comprises exposing the
 CC sample to an enzymatically non-extendable nucleobase oligomer having a
 CC nucleobase sequence complementary to a sequence within the high abundance
 CC polynucleotide under conditions so that base pairing occurs, and
 CC subjecting the sample to conditions for polymerase extension. Preferably,
 CC the enzymatically non-extendable nucleobase oligomer does not have a
 CC ribose-containing oligomeric structure. It is a peptide nucleic acid
 CC (PNA) oligomer or is a modified nucleotide oligomer or internucleotide

CC analogue oligomer. The modified nucleotide oligomer is selected from 2'-
 CC modified and 3'-modified nucleotide oligomers. The 2'-modified and 3'-
 CC modified nucleotide oligomers are selected from 2'-O-alkyl modified
 CC nucleotide oligomers and 3'-alkyl modified nucleotide oligomers. The 2'-O-
 CC -alkyl modified nucleotide oligomers are 2'-O-methyl nucleotide
 CC oligomers. The modified nucleotide oligomer or internucleotide analogue
 CC oligomer is selected from locked nucleic acids (LNA), N³-P⁵,
 CC phosphoramidate (NP) oligomers, minor groove binder-linked-
 CC oligonucleotides (MGB-linked oligonucleotides), phosphorothioate (PS)
 CC oligomers, C1-C4 alkylphosphonate oligomers, phosphoramidates, beta-
 CC phosphodiester oligonucleotides, and alpha-phosphodiester
 CC oligonucleotides. The C1-C4 alkylphosphonate oligomers are methyl
 CC phosphonate (MP) oligomers. The enzymatically non-extendable nucleobase
 CC oligomer is chimeric. The sample comprises more than one high abundance
 CC polynucleotide. The sample comprises RNA, and polymerase extension is by
 CC reverse transcription to yield a first strand cDNA. The method further
 CC comprises second strand cDNA synthesis. The sample is exposed to the
 CC nucleobase oligomer during the first and/or second strand cDNA synthesis.
 CC The method further comprises an amplification step, which is by
 CC polymerase chain reaction (PCR) or by in vitro transcription. The RNA is
 CC mRNA or cDNA or total cellular RNA. Alternatively, the sample comprises
 CC PCR. The method also comprises labelling the amplified polynucleotides.
 CC The labelling is concomitant with or subsequent to amplification. The
 CC methods are useful in selective enrichment of low abundance
 CC polynucleotides in a sample. The pool of enriched polynucleotides may be
 CC used in analysing gene expression and in creating cDNA libraries. The
 CC present sequence represents a reverse transcriptase (RT)-PCR primer which
 CC was used to amplify the human import precursor of subunit B of the H+
 CC transporting, mitochondrial ATP synthase, subunit B, isoform 1 (ATP5F1)
 CC gene.

Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAAGTAAA 1537
 21 AAAAAAAAAAAAAAAAAA 4

RESULT 941
 ABD25907
 ID ABD25907 standard; DNA; 21 BP.
 AC ABD25907;
 XX 29-JUN-2004 (first entry)
 XX A1654215-derived oligonucleotide SEQ ID 4919.
 DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiaesthetic;
 KW analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;
 KW beta-adrenergic agonists; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX Homo sapiens.
 OS WO200285309-A2.
 PN 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013143.
 PE 24-APR-2001; 2001US-0286036P.
 PR (EPIG-) EPIGENESIS PHARM INC.

XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acid associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4919; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c) the composition
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 942
ADJ88057/c
ID ADJ88057 standard; DNA; 21 BP.
XX
XX ADJ88057;
XX
XX 06-MAY-2004 (first entry)
XX
XX RT primer used in the synthesis of an artificial gene transcript.
XX
XX Selective enrichment; gene expression; RT; reverse transcriptase; primer;
KM ss.
XX
XX Unidentified.
OS
XX
XX US2004014105-A1.
XX
XX 22-JAN-2004.
PD

XX
XX 09-MAY-2003; 2003US-00435489.
XX
XX 09-MAY-2002; 2002US-00144179.
XX
XX
XX (SCHR/) SCHROEDER B G.
PA (CHEN/) CHEN C.
PA (SCHR/) SCHROTH G P.
XX
XX Schroeder BG, Chen C, Schroth GP;
PI
XX
XX WPI; 2004-121562/12.
XX
XX
XX Enriching low abundance polynucleotide relative to a high abundance
PT polynucleotide in a sample, for analyzing gene expression and creating
PT cDNA libraries, comprises blocking polymerase activity on high abundance
PT polynucleotides.
XX
XX Example 1; SEQ ID NO 41; 62pp; English.
XX
XX The present invention relates to methods for the selective enrichment of
CC low abundance polynucleotides. The invention is useful for analysing gene
CC expression in a sample and creating cDNA libraries. The present sequence
CC is reverse transcriptase (RT) primer used in the synthesis of an
CC artificial gene transcript.
XX
XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4
RESULT 943
ADM07216/c
ID ADM07216 standard; DNA; 21 BP.
XX
XX ADM07216;
XX
XX 15-JUL-2004 (first entry)
XX
XX Control primer used in cDNA first strand synthesis.
DE
XX Double-stranded cDNA synthesis; cDNA first strand synthesis;
XX cDNA second strand synthesis; RNA template; RNA amplification;
KM differential gene expression; primer; ss.
XX
XX Synthetic.
OS
XX
XX US2004081962-A1.
XX
XX 29-APR-2004.
XX
XX 23-OCT-2002; 2002US-00278760.
XX
XX 23-OCT-2002; 2002US-00278760.
XX
XX (CHEN/) CHEN C.
PA (SCHR/) SCHROEDER B.
PA (BRAN/) BRANDIS J.
PA (SCHR/) SCHROTH G.
XX
XX Chen C, Schroeder B, Brandis J, Schroth G;
PI
XX
XX WPI; 2004-340131/31.
XX
XX Synthesizing double-stranded cDNA, by synthesizing a cDNA strand from RNA
PT template, removing the template and synthesizing double-stranded cDNAs
PT using the cDNA as template in the presence of processive DNA polymerase

PT and random primers.
XX
PS Example 1, SEQ ID NO 2, 19pp; English.
XX
CC The present invention relates to a method for synthesizing double-stranded cDNA, by synthesizing first cDNA strands in a first reaction mixture complementing reverse transcriptase, RNA template, and first strand primer complementary to template, removing the template, synthesizing double-stranded cDNA in a second reaction mixture comprising processive DNA polymerase, DNA ligase, first cDNA strand as template and random primers having a mixture of oligonucleotides having random DNA sequences. Also disclosed is a method for amplifying a population of RNA molecules by synthesizing double-stranded cDNA. The generated cDNA products are useful in determining quantitative information about the genetic profile of nucleic acid in original RNA sample. The method of the invention is useful in differential gene expression assays for the analysis of diseased and normal tissue and for large-scale correlation studies on sequences, mutations, variants or polymorphisms among samples. The method is efficient in synthesizing improved cDNA molecules and effective in generating useful quantities of an amplified cDNA product that comprises a population of cRNA molecules in substantially the same relative molar ratio as the RNA or mRNA starting material. The present sequence represents a primer used for cDNA first strand synthesis.
CC
XX
SQ Sequence 21 BP, 0 A, 0 C, 0 G, 21 T, 0 U, 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4
RESULT 944
ADP09287/C
ID ADP09287 standard; DNA, 21 BP.
XX
AC ADP09287;
XX
DT 26-AUG-2004 (first entry)
XX
DE Extend primer 82 used to genotype human chromogranin B polymorphism.
XX
KM breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB; secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN W02004047767-A2.
XX
PD 10-JUN-2004.
XX
PE 25-NOV-2003; 2003WO-US037966.
XX
PR 25-NOV-2002; 2002US-0429136P.
PR 24-JUL-2003; 2003US-0490234P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Roch RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
DR WPI, 2004-441082/41.
XX
PT Identifying a subject at risk of breast cancer by detecting the presence of absence of one or more nucleotide polymorphic variations, useful for diagnosing, preventing and/or treating breast cancer.
XX
PS Example 5; Page 103; 286pp; English.
XX

CC The invention relates to a novel method for identifying a subject at risk of breast cancer which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The method of the invention has cytostatic applications and may be useful for identifying a risk of breast cancer, as well as therapeutic and prophylactic treatments that specifically target breast cancer, such as gene therapy. The current sequence is that of an extend primer of the invention which was used to genotype single nucleotide polymorphisms within human chromogranin B (CHGB; secretogranin 1; SCG1) DNA which is located at chromosomal position 20pter-p12.
XX
SQ Sequence 21 BP, 9 A, 5 C, 2 G, 5 T, 0 U, 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1311 TTTATTTTCAGACAGAGA 1328
DB 21 TTTTTTTCAGACAGAGA 4
RESULT 945
ABL60935
ID ABL60935 standard; DNA, 24 BP.
XX
AC ABL60935;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human nucleotide reducing enzyme 59.62 cDNA isolating primer 2.
XX
KM Nucleotide reducing enzyme 59.62; embryo development; teratogenesis; blood system disease; human; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1333352-A.
XX
PD 30-JAN-2002.
XX
PE 07-JUL-2000; 2000CN-00117037.
XX
PR 07-JUL-2000; 2000CN-00117037.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI, 2002-305607/35.
XX
PT Human nucleotide reducing enzyme 59.62 polypeptide and its encoding polynucleotide, for treating e.g. embryo development teratogenesis.
XX
PS Example 2; Page 17 (disclosure); 34pp; Chinese.
XX
CC The invention relates to a novel human nucleotide reducing enzyme 59.62 polypeptide and encoding polynucleotide. The polynucleotide, polypeptide and its antagonist are useful for treating e.g. embryo development teratogenesis, blood system disease, and growth development disturbance disease. The present sequence represents the human nucleotide reducing enzyme 59.62 cDNA isolating RT-PCR primer
XX
SQ Sequence 24 BP, 6 A, 2 C, 2 G, 14 T, 0 U, 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 24;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1250 TGTGTTGTTTATATCA 1267
DB 3 TTTTGTGTTTATATCA 20

```

RESULT 946
AAT69640/c
ID AAT69640 standard; DNA; 19 BP.
XX
AC AAT69640;
XX
DT 20-FEB-1998 (first entry)
XX
DE Telomerase Oligo-dT-Primer P3.
XX
KM Telomerase; substrate; primer; detection; 5'-region; retrovirus;
KM long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
KM effector compound; PCR; amplification; Oligo-dT-Primer; ss.
XX
OS Synthetic.
XX
PN DE19664302-A1.
XX
PD 05-JUN-1997.
XX
PF 24-OCT-1996; 96DE-01044302.
XX
PR 28-NOV-1995; 95DE-01044317.
XX
PA (BOEP ) BOEHRINGER MANNHEIM GMBH.
XX
PI Emrich T, Leying H, Hinzpeter M, Karl G;
DR WPI; 1997-299542/28.
XX
PT Measuring telomerase activity, useful for tumour diagnosis and compound
PT screening - by extending substrate primer, followed by amplification and
PT immobilising product for detection.
XX
PS Example; Page 11; 21pp; German.
XX
CC The present sequence is a telomerase Oligo-dT-Primer, which can be used
CC in a novel method for detecting telomerase activity. The method comprises
CC adding to a test sample a 1st primer, that serves as telomerase
CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
CC primer extension by the telomerase, amplifying the extension product,
CC immobilising the amplification product (AP) on a solid phase and
CC qualitative and/or quantitative detection of AP, where the substrate
CC primer is preferably from the 5'-region of the long terminal repeat 2
CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
CC tumours and screen compounds for effector activity. Immobilisation of AP
CC provides a signal that is reproducibly representative of telomerase
CC activity, eliminates the need for gel electrophoretic separation and
CC provides high sensitivity. Radioactive labels are not required and the
CC method can be automated for routine use. Specific detection is achieved
CC by proper choice of hybridisation conditions, without separation of the
CC telomerase extension product. A specific signal is generated by 1-10 cell
CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 5.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1518 TTTAAAAAAGTAAA 1536
Db 19 DKAAAAAAGTAAA 1
XX
RESULT 947
ADM16445/c
ID ADM16445 standard; RNA; 19 BP.
XX
AC ADM16445;
XX
XX 17-JUN-2004 (first entry)

```

```

XX
DE RNA intron poly-pyrimidine tract, seq id 2.
XX
KM Cytostatic; antimicrobial; virocid; gene therapy; RNA intron; cancer;
KM viral; microbial; infection; poly-pyrimidine tract; ds.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH 2..4
FT misc_feature /*tag= a
FT /*note= "optionally between 1-3 bases at this position"
FT misc_feature 5 /*tag= b
FT /*note= "optionally absent base"
FT misc_feature 6..17 /*tag= c
FT /*note= "optionally between 7-12 bases at this position"
FT misc_feature 19 /*tag= d
FT /*note= "optionally absent base"
XX
PN W02004024940-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029274.
XX
PR 16-SEP-2002; 2002US-0411062P.
PR 12-OCT-2002; 2002US-0418405P.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Lin S, Ying S;
XX
DR WPI; 2004-270056/25.
XX
PT New isolated RNAs comprising an intron RNA that is released in a cell,
PT thus modulating the function of a target gene, useful for treating and
PT preventing diseases such as cancer and viral/microbial infections.
XX
PS Claim 2; SEQ ID NO 2; 54pp; English.
XX
CC The invention relates to isolated RNAs comprising an intron RNA that is
CC released in a cell, thus modulating the function of a target gene. Also
CC disclosed is a DNA template for the isolated RNA, an expression vector
CC comprising the DNA, and a composition comprising one or more agents that
CC induce RNA-mediated modulation of the functions of two or more target
CC genes in a cell, such as a mammalian cell. The isolated RNAs and
CC compositions are useful for modulating the function of a target gene in a
CC cell, e.g. to inhibit a cancer-related gene, potential viral gene, and
CC microbe-related gene, and thus useful for treating and preventing
CC diseases such as cancer and viral/microbial infections. The current
CC sequence represents a potential poly-pyrimidine tract of the artificial
CC RNA intron.
XX
SQ Sequence 19 BP; 0 A; 3 C; 0 G; 0 T; 13 U; 3 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAGTAAA 1536
Db 17 AAAAAAAGRRA 1
XX
RESULT 948
AAQ75722
ID AAQ75722 standard; DNA; 21 BP.
XX
AC AAQ75722;
XX
XX

```

DT	04-AUG-1995	(first entry)
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; cDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP0630397-A.	
XX		
PD	01-NOV-1994.	
XX		
PF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.	
DR	WI; 1995-018287/03.	
XX		
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed	
PT	by digestion with restriction enzymes.	
XX		
P8	Disclosure; Page 8; 11pp; Japanese.	
XX		
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of	
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of	
CC	labelled reverse transcription primers (GENSEQ files AAQ75547-075798)	
CC	and using the aggregate of mRNAs as the template for each reverse	
CC	transcription primer; (b) digesting each of the prepared aggregates of	
CC	the double-stranded cDNAs with restriction enzyme and; (c)	
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The	
CC	method can be used to analyse gene expression rapidly and easily	
XX		
SO	Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;	
	Query Match	1.0%; Score 14.6; DB 1; Length 21;
	Best Local Similarity	81.0%; Pred. No. 4,6e+02;
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1246 TCCTTGTTGTTTTTAATC 1266	
DB	1 TTTTTTTTTTTTTTAAAC 21	
	RESULT 949	
ID	AAQ75726	
XX	AAQ75726 standard; DNA; 21 BP.	
AC		
XX	AAQ75726;	
DT		
XX	04-AUG-1995 (first entry)	
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; cDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP0630397-A.	
PN		
PD	01-NOV-1994.	
XX		
PF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.	
XX		
DR	WI; 1995-018287/03.	
XX		

```

PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 8; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENBSSO files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
OY  Query Match          1.0%; Score 14.6; DB 1; Length 21;
    Best Local Similarity 81.0%; Pred. No. 4.6e+02;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY  1246 TCCTTGGTTTGGTTTAAATC 1266
    |||||
    1 TTTTTCCTTGGTTTAAAC 21
XX
RESULT 950
AAQ75734
ID  AAQ75734 standard; DNA; 21 BP.
XX
AC  AAQ75734;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 8; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENBSSO files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
OY  Query Match          1.0%; Score 14.6; DB 1; Length 21;
    Best Local Similarity 81.0%; Pred. No. 4.6e+02;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY  1246 TCCTTGGTTTGGTTTAAATC 1266

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OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 28-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGUS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or lactic acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 1246 TCTTGTGTTGTTTATC 1266
 1 TTTTGTGTTTGTGTTTATC 21
 XX
 RESULT 954
 AAQ75762
 ID AAQ75762 standard; DNA; 21 BP.
 XX
 AC AAQ75762;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESKO files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 1246 TCTTGTGTTGTTTATC 1266
 1 TTTTGTGTTTGTGTTTATC 21
 XX
 RESULT 955
 AAQ75634
 ID AAQ75634 standard; DNA; 21 BP.
 XX
 AC AAQ75634;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX

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PS Disclosure; Page 6, 11pp, Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AA075547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1246 TCTTGTGTTGTTTAAATC 1266
DB 1 TTTTGTGTTTGTGATC 21
XX
RESULT 956
AAQ75682 standard; DNA; 21 BP.
XX
AC AAQ75682;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WP1; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7, 11pp, Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1246 TCTTGTGTTGTTTAAATC 1266
DB 1 TTTTGTGTTTGTGATC 21
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RESULT 957
AAQ75753/c
ID AAQ75753 standard; DNA; 21 BP.
XX
AC AAQ75753;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WP1; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8, 11pp, Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESKO files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1510 ACTGTTAATTAAAAAAA 1530
DB 21 ACTGAAAAA 1
XX
RESULT 958
AAQ75764
ID AAQ75764 standard; DNA; 21 BP.
XX
AC AAQ75764;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
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XX 16-APR-1993; 93JP-00112515.
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1302 TCTATTTTATTTTATTTTCAGA 1322
DB 1 TTTTATTTTATTTTATTTTCACA 21
XX
XX RESULT 959
XX AAQ75714
XX ID AAQ75714 standard; DNA; 21 BP.
XX
XX AAQ75714;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
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```
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1246 TCTTTGTTTGTATTTTATTC 1266
DB 1 TTTTATTTTATTTTATTTTATTC 21
XX
XX RESULT 960
XX AAQ75760
XX ID AAQ75760 standard; DNA; 21 BP.
XX
XX AAQ75760;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1302 TCTATTTTATTTTATTTTCAGA 1322
DB 1 TTTTATTTTATTTTATTTTTCACA 21
XX
XX RESULT 961
XX AAQ75756
XX ID AAQ75756 standard; DNA; 21 BP.
XX
XX AAQ75756;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
```

```
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1302 TCTATTTTATTTTATTTTCA 1322
XX 1 TTTTATTTTATTTTATTTTCA 21
XX
XX Db
XX
XX RESULT 962
XX AAQ75698
XX ID AAQ75698 standard; DNA; 21 BP.
XX
XX AC AAQ75698;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
```

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XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1246 TCTTGTGTTGTTTATTAAC 1266
XX 1 TTTTATTTTATTTTATTTACTC 21
XX
XX Db
XX
XX RESULT 963
XX ABA93238/C
XX ID ABA93238 standard; DNA; 22 BP.
XX
XX AC ABA93238;
XX
XX DT 18-APR-2002 (first entry)
XX
XX DE Polya adaptor oligonucleotide SEQ ID NO:1.
XX
XX KM Detection; comparative detection; adaptor; ss.
XX
XX OS Synthetic.
XX
XX PN JP2001333800-A.
XX
XX PD 04-DEC-2001.
XX
XX PF 30-MAY-2000; 2000JP-00160324.
XX
XX PR 30-MAY-2000; 2000JP-00160324.
XX
XX (UNIT-) UNITECH CO LTD.
XX
XX WPI; 2002-135950/18.
XX
XX Comparative detection of the amounts of RNA and DNA.
XX
XX Disclosure; Page 9; 9pp; Japanese.
XX
XX The present invention describes a method for the comparative detection of
XX the amount of an RNA. The method comprises: (a) cDNAs obtained by
XX transcribing respectively from at least two tissue RNAs are respectively
XX fragmented by using a same restriction enzyme; (b) each different adaptor
XX and a common adaptor are added to each of the cDNA fragments derived from
XX the same or different tissues by the step (a); (c) the resultant adaptor-
XX added cDNAs are mixed together; (d) an adaptor primer having the common
XX sequence to said different adaptor and a gene-specific adaptor are used
XX to amplify said adaptor-added cDNAs containing no region derived from
XX polyadenylic acid of the mRNA before the addition of the adaptor among
XX the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
XX cDNA amounts are measured between the tissues; (f) the RNA is detected
XX from the measured result; (g) each different adaptor and a common adaptor
XX are added to each of the genomic DNA fragments derived from a same or
XX different individuals; (h) the resultant adaptor-added genomic DNAs are
XX mixed together; (i) the adaptor-added genomic DNAs are amplified by using
XX an adaptor primer having the common sequence to the different adaptor and
XX a sequence-specific adaptor; and (j) the ratios of the amplified amounts
XX of the genomic DNAs are measured between the individuals. The method is
XX used for the detection of the amounts of RNA and DNA. The present
XX sequence represents an oligonucleotide which is used in the
XX exemplification of the present invention
```

```
XX Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1246 TCTTGGTTGTTTATC 1266
DB 21 TTTTGTGTGTGTGTATC 1

RESULT 964
ABK6361
ID ABK6361 standard; DNA; 24 BP.
XX
AC AA16361;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human phosphatidylinositol-3 kinase 35 CDNA PCR primer #2.
XX
KW Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175014-A2.
XX
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN000328.
XX
PR 17-MAR-2000; 2000CN-00114973.
XX
PA (BIOV-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-025836/03.
XX
PT New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer; haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1302 TCTATTTTATTTTATTCAGA 1322
DB 4 TTTTGTGTGTGTGTATTAAGA 24

RESULT 965
ABK6169/C
ID ABK6169 standard; DNA; 24 BP.
XX
AC ABK6169;
XX
DT 24-SEP-2002 (first entry)
XX
```

```
DE Oligo dT primer #2 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Disclosure; Page 11; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dT primer used in the method of the
XX
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1246 TCTTGGTTGTTTATC 1266
DB 21 TTTTGTGTGTGTGTATTAAC 1

RESULT 966
ABK6168
ID ABK6168 standard; DNA; 24 BP.
XX
AC ABK6168;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #1 used in method to study gene expression.
XX
```

KW Oligo dt primer; gene expression analysis; primer; ss.
XX Synthetic.
OS
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
PI Kane MD, Dombkowski AA, Nagel AC;
XX WPI; 2002-508123/54.
XX
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNA expressed at different levels, comprises employing an
PT primer having an oligo-dt primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
XX
PS Disclosure; Page 11; 45pp; English.
XX
XX The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dt primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given *in vivo* or *in vitro* RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level; (c) determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dt primer used in the method of the
CC invention
XX
SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other:
XX
Query Match 1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1246 TCTTGGTTGGTTTAAATC 1266
DB 4 TTTTTTTTTTTTTTTAAAC 24

RESULT 967
ADB04575/c
ID ADB04575 standard; DNA; 25 BP.
XX
AC ADB04575;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5561.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
PN EP1281758-A2.
XX
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
PA Shannon M, Gu Y, Nguyen C;
PI WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5561; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other:
XX
Query Match 1.0%; Score 14.6; DB 1; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1512 TGTTAATTAAAAAANAAG 1532
DB 21 TCTCAAAAAAAAAAAAAAAG 1

RESULT 968
AAN50186/c
ID AAN50186 standard; DNA; 16 BP.
XX
AC AAN50186;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1991 (first entry)
XX
DE Sequence of human immunoglobulin gene enhancer region called unit E1.
XX
KW Immunoglobulin gene; enhancer; promoter; expression cassette; ss.
XX
OS Homo sapiens.
XX
PN EP146743-A.
XX
PD 03-JUL-1985.
XX
XX 06-NOV-1984; 84EP-00113371.
PF

```
XX 08-NOV-1993; 83JP-00208383.
PR 06-DEC-1993; 83JP-00229037.
PR 04-JUN-1994; 84JP-00113047.
PR 05-JUN-1994; 84JP-00113834.
XX
XX (TEIJ ) TEIJIN LTD.
PI Kudo A, Nakamura S, Suni Y, Ichikawa Y, Matanabe T;
XX
XX WPI; 1985-160489/27.
DR
XX Fragments derived from chromosomal DNA of human immunoglobulin gene -
PT useful in transcription and translation procedures.
XX
XX Claim 10; Page 34; 49pp; English.
XX
XX The inventors claim a gene fragment comprising (a) the enhancer DNA
CC segment and (b) a structural gene such as human D, V and J gene, and a
CC promoter. Using the gene fragments of the invention, transcription and
CC translation efficiency are enhanced. (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 16 BP; 5 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1514 TTAATTAAAAAAA 1529
DB 16 TTAATTAAAAAATTA 1
RESULT 969
AAK69795/C
ID AAK69795 standard; RNA; 17 BP.
XX
XX AAK69795;
AC
XX 28-JUN-1999 (first entry)
DT
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1090.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fme-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX 25-OCT-1996; 96WO-US017480.
PE
XX 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
```

```
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fme-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK67275 to AAK75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 3 C; 0 G; 0 T; 13 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1521 AAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAAGTGA 2
RESULT 970
AAA21311/C
ID AAA21311 standard; RNA; 17 BP.
XX
XX AAA21311;
AC
XX 19-JUN-2000 (first entry)
DT
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4537.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosstatic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KM tubercous sclerosis; pct-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9950403-A2.
PN
XX
XX 07-OCT-1999.
PD
XX 24-MAR-1999; 99WO-US006507.
PE
XX 27-MAR-1998; 98US-0079678P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 55; Page 200; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17621 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
```

```
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23342 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 5 A; 2 C; 0 G; 0 T; 10 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1512 TGTAAATTAAAAAAA 1527
DB 17 TGTAAATTAAAAAAA 2
XX
XX AAA21312;
XX
XX AC
XX
XX ID AAA21312 standard; RNA; 17 BP.
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4538.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioidibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN MO9950403-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 24-MAR-1999; 99WO-US006507.
XX
XX PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX
XX DR WPI; 1999-591315/50.
XX
XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX PS Claim 55; Page 200; 305pp; English.
XX
XX CC The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a tie-2 gene. AAA16775 to
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CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23342 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 2 C; 0 G; 0 T; 11 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1512 TGTAAATTAAAAAAA 1527
DB 16 TGTAAATTAAAAAAA 1
XX
XX AC
XX
XX ID AAV91364 standard; RNA; 17 BP.
XX
XX AC AAV91364;
XX
XX DT 18-FEB-1999 (first entry)
XX
XX DE Human C-raf target site nucleotide position 2745.
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalytic; modulation; expression; Raf gene; delivery;
XX screening; identification; synthesis; deprotection; purification; cancer;
XX inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX restenosis; rheumatoid arthritis; ss.
XX
XX
XX OS
XX PN MO9850530-A2.
XX
XX PD 12-NOV-1998.
XX
XX PF 05-MAY-1998; 98WO-US009249.
XX
XX PR 09-MAY-1997; 97US-0046059P.
XX
XX PR 09-JUN-1997; 97US-0049002P.
XX
XX PR 03-JUL-1997; 97US-0051718P.
XX
XX PR 22-AUG-1997; 97US-0056808P.
XX
XX PR 02-OCT-1997; 97US-0061321P.
XX
XX PR 02-OCT-1997; 97US-0061324P.
XX
XX PR 05-NOV-1997; 97US-0064866P.
XX
XX PR 19-DEC-1997; 97US-0068212P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PA Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX
XX PI Parry T, Bigelman L, Mcswigen JA, Karpelsky A, Burgin A;
XX
XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX DR WPI; 1999-009494/01.
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```
XX
PT - especially new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT - restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
PS Claim 177, Page 153, 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in a system where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC acetos and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
CC
XX
SQ Sequence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 806 TGCTGAATTTGTGTT 821
DB 1 UGCGAATUUUUGUCUU 16
XX
RESULT 973
AAZ38362/C
ID AAZ38362 standard; DNA; 17 BP.
XX
AC AAZ38362;
XX
DT 15-FEB-2000 (first entry)
XX
DE SPl consensus binding element.
XX
KW SPl; consensus; competition gel mobility shift assay; apolipoprotein AI;
KW apo AI; low density lipoprotein; LDL; cholesterol;
KW coronary artery disease; promoter; flanking region; plasmid; DRE;
KW drug responsive element; reporter gene; drug screening; candidate;
KW expression; identification; rapid; automation; enhancer; element; ds.
XX
OS Synthetic.
XX
PN US5994061-A.
XX
PD 30-NOV-1999.
XX
PF 29-SEP-1995; 95US-00536559.
XX
PR 29-SEP-1995; 95US-00536559.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Tam S, Zhang X;
XX
DR WPI; 2000-038251/03.
XX
PT Screening for drugs that increase expression of the apolipoprotein AI
PT gene, which may then be useful for treating coronary artery disease.
```

```
XX
PS Example 7, Col 23-24; 38pp; English.
XX
CC Sequences AAZ38358-238364 represent double-stranded oligonucleotide
CC probes which comprise various different enhancer elements. These were
CC used as competitor probes in competition gel mobility shift assays
CC performed to determine the specificity of drug-inducible nuclear proteins
CC to a fragment of the 5' flanking region of the human apolipoprotein AI
CC (apo AI) gene comprising the sequence between bases -79 and -44 from the
CC transcription start site (AAZ38357). This apo AI fragment contains two
CC DRs (AAZ38355, AAZ38356) in opposite orientations, and was used in the
CC construction of plasmids pGL2 (apoAI-DRE)/TK/luc (AAZ38352), which
CC contains one copy of this fragment, and pGL2 (4xapoAI-DRE)/TK/luc
CC (AAZ38353) which contains four copies. The promoter and luciferase
CC upstream of the HSV thymidine kinase (TK) promoter and luciferase
CC reporter gene in the pGL2 TK/luc vector. The pGL2 TK/luc vector also
CC comprises a functional polyadenylation sequence downstream of the
CC reporter gene. Plasmid pGL2 (apoAI-DRE)/TK/luc and pGL2 (4xapoAI-
CC DRE)/TK/luc are used in a novel method for screening for a drug that
CC increases expression of a gene for apolipoprotein (apo AI), which is
CC associated with coronary artery disease. Such plasmids may be transformed
CC into mammalian cells, which are treated with a candidate compound, lysed
CC and assayed for reporter gene activity relative to extracts from
CC untreated cells. The method is useful for screening and identifying drugs
CC that increase apo AI gene expression, the identified drugs would be
CC useful for treating coronary artery disease. The method is simple, rapid,
CC and lends itself to automation
XX
SQ Sequence 17 BP; 2 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 345 CTGCGCCGCCCGCAG 360
DB 16 CTGCCCCGCCCGCAG 1
XX
RESULT 974
AAA25444/C
ID AAA25444 standard; DNA; 17 BP.
XX
AC AAA25444;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1942.
XX
KW Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphothioate; endonuclease;
KW anticancer; breast cancer; endometrial cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
XX
PA 23-JUN-1998; 98US-00103636.
XX
PI (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Belgelman L, Meswigen JA, Karpelesky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Heberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
```


PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1521 AAAAAAAAAAGTAA 1536
DB 17 AAAAAAAAAAACTAA 2
XX
RESULT 975
AAA25446/C
ID AAA25446 standard; DNA; 17 BP.
XX
AC AAA25446;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.
XX
KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN MO9954459-A2.
XX
PD 28-OCT-1999.
XX
PE 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelisky A, Bellon L,
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P,
PI Matulic-Adamic J;
XX
DR WPI; 2000-013246/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.

XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1535
DB 16 AAAAAAAAAAACTAA 1
XX
RESULT 976
AAF06141
ID AAF06141 standard; DNA; 17 BP.
XX
AC AAF06141;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2938.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PE 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 42; Page 123; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the Trk Orphan receptor, EGR3/CODP-TF-1, the GATA transcription

```
CC factor gene, IRF-2 and/or the CAA/T Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 0 A; 1 C; 4 G; 0 T; 12 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 6.2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Oy 1247 CTTGTTTGTGTTT 1262
|::|::|::|::|::|
Db 1 CUUGUUUUUUUUUU 16

RESULT 977
AAF06140
ID AAF06140 standard; DNA; 17 BP.
XX
AC AAF06140;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2937.
XX
KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Zwick M, Pavco P, Mcawiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
XX
PS Claim 42; Page 123; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAA/T Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 0 A; 1 C; 4 G; 0 T; 12 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 6.2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Oy 1247 CTTGTTTGTGTTT 1262
|::|::|::|::|::|
Db 2 CUUGUUUUUUUUUU 17

RESULT 978
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ABN01468/C
ID ABN01468 standard; DNA; 17 BP.
XX
AC ABN01468;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1460.
XX
KM Human, genome-derived myosin-like protein 1; GDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 1460; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
```

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 332 TTCCGAGAGCTCTG 347
DB 16 TTCCGAGAGCTGCTG 1

RESULT 979
ABN01467/c
ID ABN01467 standard; DNA; 17 BP.
XX
AC ABN01467;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1459.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KV muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 1459; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX

Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 332 TTCCGAGAGCTCTG 347
DB 17 TTCCGAGAGCTGCTG 2

RESULT 980
ABN02279/c
ID ABN02279 standard; DNA; 17 BP.
XX
AC ABN02279;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2271.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KV muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2271; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-

CC	1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC	nucleic acids can be used as probes to detect, characterise and quantify
CC	hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC	provide initial substrates for the recombinant engineering of hGDMLP-1
CC	protein variants having desired phenotypic improvements, and for
CC	expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC	used as immunogens to raise antibodies that specifically recognise hGDMLP-
CC	-1 proteins, as standards in assays used to determine the concentration
CC	and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC	capture probes for surface-enhanced laser desorption/ionisation, as
CC	therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC	production, and in vaccines or for replacement therapy. The
CC	polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC	disorder associated with the expression of hGDMLP-1, in particular heart
CC	and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC	The present sequence represents an oligomer used in the screening of the
CC	hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequence
SX	
SO	Sequence 17 BP; 0 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match	1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity	93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
OY	396 GCCGAGGCCCGCAGC .411 16 GCCGAGGCCCGCAGC 1
Dd	
RESULT 981	
ID	ABN02278/c
XX	ABN02278 standard; DNA; 17 BP.
AC	
XX	ABN02278;
DT	
XX	29-MAY-2002 (first entry)
DE	
XX	Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2270.
KM	Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX	skeletal muscle disorder; amplicon; screening; ss.
OS	
XX	Homo sapiens.
PN	
XX	WO200192524-A2.
PD	
XX	06-DEC-2001.
Pf	
XX	25-MAY-2001; 2001WO-US016981.
PR	
XX	26-MAY-2000; 2000US-0207456P.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024253.
PR	30-JAN-2001; 2001WO-US000651.
PR	30-JAN-2001; 2001WO-US000652.
PR	30-JAN-2001; 2001WO-US000653.
PR	30-JAN-2001; 2001WO-US000654.
PR	30-JAN-2001; 2001WO-US000655.
PR	30-JAN-2001; 2001WO-US000656.
PR	30-JAN-2001; 2001WO-US000657.
PR	30-JAN-2001; 2001WO-US000658.
PR	30-JAN-2001; 2001WO-US000659.
PR	30-JAN-2001; 2001WO-US000670.
PR	05-FEB-2001; 2001US-0266860P.
XX	
PA	(AEOM-) AEOMICA INC.
XI	
Gu Y,	Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX		WP; 2002-179446/23.
XX		
XR		New polypeptide, for raising antibodies that recognise hGDMLP-1 proteins,
PT		or as specific biomolecule capture probes for surface-enhanced laser
PT		desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX		
PS		Disclosure; SEQ ID NO 2270; 214pp; English.
XX		
CC	The present invention describes a human genome-derived myosin-like	
CC	protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-	
CC	1 can be used in gene therapy and vaccine production. The hGDMLP-1	
CC	nucleic acids can be used as probes to detect, characterise and quantify	
CC	hGDMLP-1 nucleic acids in samples, as amplification substrates, to	
CC	provide initial substrates for the recombinant engineering of hGDMLP-1	
CC	protein variants having desired phenotypic improvements, and for	
CC	expressing the protein. The hGDMLP-1 proteins or polypeptides may be	
CC	used as immunogens to raise antibodies that specifically recognise hGDMLP	
CC	-1 proteins, as standards in assays used to determine the concentration	
CC	and/or amount specifically of hGDMLP proteins, as specific biomolecule	
CC	capture probes for surface-enhanced laser desorption/ionisation, as	
CC	therapeutic supplement in patients having specific deficiency in hGDMLP-1	
CC	production, and in vaccines or for replacement therapy. The	
CC	polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a	
CC	disorder associated with the expression of hGDMLP-1, in particular heart	
CC	. and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.	
CC	The present sequence represents an oligomer used in the screening of the	
CC	hGDMLP-1 sequence in the exemplification of the present invention. N.B.	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequence	
SQ	Sequence 17 BP; 0 A; 8 C; 5 G; 4 T; 0 U; 0 Other;	
XX		
Oy	Query Match 1.0%; Score 14.4; DB 1; Length 17;	
	Best Local Similarity 93.8%; Pred. No. 6.2e+02;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Db	396 GCCGAAGCGCCGCAGG 411 17 GCCGAAGCGCCGCAGG 2	
ACNI2480		
ID ACN12480 standard; RNA; 17 BP.		
XX ACN12480;		
XX AC		
DT 22-APR-2004 (first entry)		
DE MNV minus strand Zinzyme substrate SEQ ID NO 12483.		
KM MNV, West Nile Virus; anti-inflammatory; cytosolic; hepatotropic; viral; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss. West Nile Virus. WO200268637-A2. 06-SEP-2002. 19-OCT-2001; 2001MO-USO48350. 20-OCT-2000; 2000US-024241P. (RIBO-) RIBOZYME PHARM INC. (BLAT/) BLATT L. (MCSSW/) MCSWIGGEN J A.		

PI Blact L, Mcswigen JA;
XX WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 12483; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 6.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1544 GCAGATGTCACCCAG 1559
Db 2 GCAGAGUUAACCCAG 17
XX
RESULT 983
ID ACN01139 standard; RNA; 17 BP.
XX
AC ACN01139;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Hammerhead Ribozyme substrate SEQ ID NO 1129.
XX
KM WNV; West Nile Virus; antiinflammatory; cytoprotatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KM Amberzyme; Zinzyne; ss.
XX
OS West Nile Virus.
XX
XX W0200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blact L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PT

XX
XX Claim 23; SEQ ID NO 1129; 495bp; English.
XX
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 6.2e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
XX
QY 696 CGCTGTGAATGAGT 711
Db 2 CGCUGGUAUGGAGU 17
XX
RESULT 984
ID ACN01209/c standard; RNA; 17 BP.
XX
AC ACN01209;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Hammerhead Ribozyme substrate SEQ ID NO 1199.
XX
XX
KM WNV; West Nile Virus; antiinflammatory; cytoprotatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KM Amberzyme; Zinzyne; ss.
XX
OS West Nile Virus.
XX
XX W0200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blact L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PT
XX
XX Claim 23; SEQ ID NO 1199; 495bp; English.
XX
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1544 GCAGGATGTCACCCAG 1559
DB 17 GCAGGATGTCACCCAG 2
RESULT 985
ACN14420/C
ID ACN14420 standard; RNA; 17 BP.
XX
AC ACN14420;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV minus strand Amberzyme substrate SEQ ID NO 14423.
XX
OS MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;
KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PE 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blact L, Mcswigen JA;
PI
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 14423; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 696 CGCTGTGATGAGT 711
DB 16 CGCTGTGATGAGT 1
RESULT 986
ACN03016
ID ACN03016 standard; RNA; 17 BP.
XX
AC ACN03016;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme substrate SEQ ID NO 3019.
XX
XX
OS MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;
KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PE 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blact L, Mcswigen JA;
PI
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 3019; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 6.2e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 696 CGCTGCGATGAGT 711
|||:|:|:|:|:|:|:
Db 1 CGCUGGCAUGAGU 16

RESULT 987

ACN07859/c
ID ACN07859 standard; RNA; 17 BP.

AC ACN07859;

DT 22-APR-2004 (first entry)

XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7862.

XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-024241P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PI (MCSW/) MCSWIGEN J A.

PI Blatt L, Mcswigen JA;

XX WPI: 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis,

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7862; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for

XX treating a condition related to MNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

RESULT 988

ABT36080/c
ID ABT36080 standard; DNA; 17 BP.

AC ABT36080;

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID NO 1717.

XX Cytostratic; virucide; neuroprotective; nocitropic; neuroleptic; gene chip;

KW antisense; senesc; tumour; cell degeneration; cancer; Alzheimer's disease;

KW schizophrenia; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI: 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; Page 233; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX given in the specification, a sequence containing at least 15 consecutive

XX nucleotides from the 17 mer sequence, a sequence with, after optional

XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that

XX hybridizes to them under highly stringent conditions, or the complement

XX of any of them, or the corresponding RNA. The novel isolated nucleic

XX acids of the invention are useful as probes and primers for detecting,

XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX component of a gene chip, in vitro as (anti)sense reagents, and for

XX production of recombinant polypeptides. Any of the nucleic acids,

XX polypeptides, vectors containing the nucleic acids, cells containing the

XX vector or antibodies directed against the polypeptides are useful for

XX preparation of pharmaceuticals for prevention and/or treatment of viral

XX diseases that are characterised by development of tumours or cell

XX degeneration, specifically cancer but also Alzheimer's disease and

XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

XX patient samples is useful for diagnosis and/or prognosis of these

Query Match

Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1315 TTTTCAGAGCAGATC 1330
|||||:|:|:|:|:|:|:
Db 16 TTTTCAGAGCAGATC 1

RESULT 989

ACN07859/c

AC ACN07859;

DT 22-APR-2004 (first entry)

XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7862.

XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-024241P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PI (MCSW/) MCSWIGEN J A.

PI Blatt L, Mcswigen JA;

XX WPI: 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis,

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7862; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for

XX treating a condition related to MNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

ID	ABT35552	ABT35552 standard; DNA; 17 BP.
XX	ABT35552;	
AC	ABT35552;	
XX	12-JUN-2003 (first entry)	
DT		
XX		
DE	Tumour suppression related human fukutin oligo SEQ ID No 1189.	
KX	Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;	
KW	antigenase; sense; tumour; cell degeneration; cancer; Alzheimer's disease;	
KW	schizophrenia; protein chip; gene therapy; tumour suppression;	
KW	human fukutin; de.	
XX		
OS	Homo sapiens.	
XX		
PN	MO2003025175-A2.	
XX		
PD	27-MAR-2003.	
XX		
XX	17-SEP-2002; 2002MO-IB004208.	
PP		
XX	17-SEP-2001; 2001FR-00011978.	
PR		
XX	(MOLE-) MOLECULAR ENGINES LAB.	
PA		
PI	Tejerman A, Amson R, Tuijnder M;	
XX		
XX	WPI; 2003-313353/30.	
DR		
XX		
PT	New isolated nucleic acid, useful for treating viral diseases associated	
PT	with tumors and cell degeneration, also related polypeptides, antibodies	
PT	and transfected cells.	
XX		
PS	Disclosure; Page 172; 720pp; French.	
XX		
CC	The invention relates to a novel isolated 17 mer nucleic acid sequence,	
CC	given in the specification, a sequence containing at least 15 consecutive	
CC	nucleotides from the 17 mer sequence, a sequence with, after optimal	
CC	alignment, at least 80 % identity to the 17 mer sequence, a sequence that	
CC	hybridizes to them under highly stringent conditions, or the complement	
CC	of any of them, or the corresponding RNA. The novel isolated nucleic	
CC	acids of the invention are useful as probes and primers for detecting,	
CC	identifying, quantifying and/or amplifying a nucleic acid, e.g. as one	
CC	component of a gene chip, in vitro as (antisense reagents, and for	
CC	production of recombinant polypeptides. Any of the nucleic acids,	
CC	polypeptides, vectors containing the nucleic acids, cells containing the	
CC	vector or antibodies directed against the polypeptides are useful for	
CC	preparation of pharmaceuticals for prevention and/or treatment of viral	
CC	diseases that are characterized by development of tumours or cell	
CC	degeneration, specifically cancer but also Alzheimer's disease and	
CC	schizophrenia. Analysis of the expression of the 17 mer nucleic acids in	
CC	patient samples is useful for diagnosis and/or prognosis of these	
CC	diseases. The polypeptides can also be used to generate antibodies, and	
CC	both the polypeptide and antibodies are useful as components of protein	
CC	chips. The nucleic acid sequences of the invention can be used in gene	
CC	therapy. This polynucleotide sequence represents a tumour suppression	
CC	related human fukutin oligonucleotide of the invention	
XX		
XX	Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;	
SO		
Query Match	1.0%; Score 14.4; DB 1; Length 17;	
Best Local Similarity	93.8%; Pred. No. 6.2e+02;	
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Oy	1348 ATTTTATTTTCCCTT 1363	
Db	2 ATCTTATTTTCCCTT 17	
RESULT	990	
ID	AB264551/C	
ID	AB264551 standard; RNA; 17 BP.	

XX	AB264551;
XX	
XX	21-MAR-2003 (first entry)
XX	
XX	Human HER2 DNAzyme substrate #8.
XX	
XX	Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX	enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX	anti-rheumatic; cancer; AIDS; ss.
XX	
XX	Homo sapiens.
XX	
XX	WO200297114-A2.
XX	
XX	05-DEC-2002.
XX	
XX	29-MAY-2002; 2002WO-US016840.
XX	
XX	29-MAY-2001; 2001US-0294140P.
XX	06-JUN-2001; 2001US-0296249P.
XX	10-SEP-2001; 2001US-0318471P.
XX	
XX	(RIBO-) RIBOZYME PHARM INC.
XX	
XX	Mcawiggen J;
XX	
XX	WPI; 2003-140484/13.
XX	
XX	Novel short interfering RNA and enzymatic nucleic acid useful for
XX	treating cancer, modulates the expression of a nucleic acid encoding
XX	HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX	
XX	Claim 4; Page 133; 185pp; English.
XX	
XX	The invention relates to a novel short interfering RNA (siRNA) nucleic
XX	acid molecule or an enzymatic nucleic acid molecule, that modulates
XX	expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX	human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX	acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX	rheumatic activity. The nucleic acid molecules are useful for reducing
XX	HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX	also useful for treating breast, ovarian, colorectal, lung, prostate,
XX	bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX	shown in AB259889 - AB262216, AB264544 - AB265531, AB265520 - AB265524,
XX	AB265530 - AB265585 represent substrate/target sequences for the human
XX	ribozymes of the invention
XX	
XX	Sequence 17 BP, 1 A, 9 C, 7 G, 0 T, 0 U, 0 Other;
XX	
XX	Query Match 1.0%; Score 14.4; DB 1; Length 17;
XX	Best Local Similarity 93.8%; Pred. No. 6.2e+02;
XX	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
XX	
XX	469 GGGGCGCGGGCTGAC 484
XX	
XX	17 GGGGCGCGGGCTGCC 2
XX	
XX	RESULT 991
XX	ACD60861/C
XX	ID ACD60861 standard; RNA; 17 BP.
XX	
XX	ACD60861;
XX	
XX	24-SEP-2003 (first entry)
XX	
XX	HCV DNAzyme substrate sequence #2047.
XX	
XX	Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX	RNA stability; RNA expression; RNA synthesis; antisense;
XX	enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinozyme;
XX	amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;

KM HBV reverse transcriptase; Enhancer I region; viral replication;
KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KM liver failure; hepatocellular carcinoma; hepatocytic; cytostatic;
KM virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
XX
PR 08-JUN-2001; 2001US-00877478.
XX
PR 08-JUN-2001; 2001US-0296876P.
XX
PR 24-OCT-2001; 2001US-0335058P.
XX
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PA (BLAT/) BLATT L.
XX
PA (MACE/) MACEJAK D.
XX
PA (MCSM/) MCSWIGEN J.
XX
PA (MORC/) MORRISSEY D.
XX
PA (PAVC/) PAVCO P.
XX
PA (LEEP/) LEE P.
XX
PA (DRAP/) DRAPER K.
XX
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 270; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinczymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 7 C; 7 G; 0 T; 2 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 961 TCGCGCGCGCGCGCG 976
DB 17 TCGCGCGCGCGCGCG 2
RESULT 992
ADB44694
ID ADB44694 standard; DNA; 17 BP.

XX ADB44694;
AC 18-DEC-2003 (first entry)
XX
DT
XX
DE Tumour suppression/reversion associated nucleotide #5017.
XX
KM cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumours and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 618; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptides are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analyses of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1348 ATTTTATTTTCCCTT 1363
DB 2 ATCTTATTTTCCCTT 17
RESULT 993
ACC54422
ID ACC54422 standard; DNA; 17 BP.
XX
AC ACC54422;
XX
DT 27-JUN-2003 (first entry)

```
XX DE Human tumour suppressor sequence #3189.
XX XX
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX XX
XX FN FR2826373-A1.
XX XX
XX PD 27-DEC-2002.
XX XX
XX PE 20-JUN-2001; 2001FR-00008139.
XX XX
XX PR 20-JUN-2001; 2001FR-00008139.
XX XX
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX DR
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 776; 798pp; French.
XX XX
XX CC This sequence represents an isolated nucleic acid sequence associated
XX CC with tumour suppression or regression, apoptosis or virus resistance. The
XX CC invention relates to these sequences or sequences having at least 80%
XX CC identity to them, and polypeptides encoded by the sequences or
XX CC polypeptides having 80% identity to the polypeptide sequences. The
XX CC invention is used to diagnose or treat viral disease or disease
XX CC characterized by development of tumour cells or cellular degeneration
XX CC
XX SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 6.2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1348 ATTTTATTTCCCTT 1363
DB 2 ATCTTATTTCCCTT 17
XX
XX RESULT 994
XX AD184801/C
XX ID AD184801 standard; RNA; 17 BP.
XX AC
XX AD184801;
XX DT 03-JUN-2004 (first entry)
XX DE HCV DNAzyme substrate sequence #2047.
XX XX
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
XX KW HCV infection; type I interferon; DNAzyme.
XX OS Hepatitis C virus.
XX XX
XX FN US2003125270-A1.
XX PD 03-JUL-2003.
XX XX
XX PE 18-DEC-2000; 2000US-00740332.
XX XX
XX PR 18-DEC-2000; 2000US-00740332.
XX XX
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGEN J.
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PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX XX
XX PI Blatt L, Mcswigen J, Roberts E, Pavco PA, Macejack D;
XX DR WPI; 2004-031273/03.
XX XX
XX PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
XX PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
XX PT especially in combination with type I interferon therapy.
XX PS Claim 1; SEQ ID NO 2047; 198pp; English.
XX XX
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
XX CC the binding arms of the enzymatic nucleic acid molecule comprises
XX CC sequences complementary to any of the defined substrate sequences given
XX CC in the specification. The nucleic acid molecule may be administered for
XX CC the treatment of HCV infections, especially in combination with type I
XX CC interferons. The present sequence represents a HCV DNAzyme substrate
XX CC sequence.
XX SQ Sequence 17 BP; 1 A; 7 C; 7 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 6.2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 961 TCGCGCGGCCCCGCG 976
DB 17 TCGCGCGGCAACGCG 2
XX
XX RESULT 995
XX AAA92546/C
XX ID AAA92546 standard; DNA; 18 BP.
XX AC
XX AAA92546;
XX DT 04-JAN-2001 (first entry)
XX DE Antisense oligonucleotide ISIS# 30213.
XX KW Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
XX KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
XX OS Synthetic.
XX PN US6107092-A.
XX PD 22-AUG-2000.
XX PE 29-MAR-1999; 99US-00280409.
XX PR 29-MAR-1999; 99US-00280409.
XX PA (ISIS-) ISIS PHARM INC.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PI Cowsett LM, Bennett CF, O'malley BW;
XX WPI; 2000-586211/55.
XX DR
XX PT Antisense compounds targeted to steroid receptor RNA activator useful for
XX PT diagnosis, prophylaxis and treatment of diseases associated with the
XX PT steroid activator, such as infection, inflammation or tumor formation.
XX PS Claim 3; Col 41; 47pp; English.
XX XX
XX CC The present sequence is one of a large number of antisense
XX CC oligonucleotides which is directed against one of four human steroid
XX CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
```



```
CC Invention
XX Sequence 18 BP; 4 A; 2 C; 0 G; 12 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1514 TTAATTAATAAAAAA 1529
Db 16 TGAATTAATAAAAAA 1

RESULT 998
AD120873 standard; DNA; 18 BP.
XX AD120873;
XX AD120873;
XX 06-MAY-2004 (first entry)
XX MS SnuPE detection oligonucleotide for DD3 #13.
XX DD3; CPG dinucleotide; cell proliferative disorder; ss.
XX Synthetic.
XX WO2004005543-A1.
XX 15-JAN-2004.
XX 25-JUN-2003; 2003WO-EP006690.
XX 08-JUL-2002; 2002DE-01030692.
XX (EPIC-) EPIDENOMICS AG.
XX PA
XX PI Horns T;
XX WPI; 2004-091385/09.
XX
XX Detecting methylation of 5' and promoter region of DD3 gene for
XX diagnosing proliferative disorders comprising contacting target nucleic
XX acid with a reagent that distinguishes between methylated and non-
XX methylated CPG dinucleotide.
XX
XX Claim 6; SEQ ID NO 76; 56bp; English.
XX
XX The present invention relates to detecting the methylation state of the
XX 5' and promoter region of the gene DD3 within a subject comprising
XX contacting a target nucleic acid having one or more sequences selected
XX from 5 3581 base pair sequences in a biological sample with at least one
XX reagent or a series of reagents. The method is useful for detecting the
XX methylation state of the 5' and promoter region of the gene DD3 within a
XX subject. The set of oligonucleotides comprising at least three of the
XX oligomers is useful for detecting the cytosine methylation state and/or
XX single nucleotide polymorphisms (SNPs) within SEQ. ID NO. 1-5 and its
XX complementary sequences. The set of oligomers is also useful for
XX detecting the methylation state of all CPG dinucleotides within SEQ ID
XX NO. 1 and its complementary sequences. The set of at least two
XX oligonucleotides can be used as primer oligonucleotides for the
XX amplification of DNA sequences selected from SEQ ID NO. 1-5 and its
XX complementary sequences. The DNA- and/or PNA-array is useful for
XX analyzing diseases associated with the methylation state of the gene DD3
XX comprising at least one nucleic acid. The methods, nucleic acids,
XX oligonucleotide or PNA-oligomer, kit, array or the set of
XX oligonucleotides is useful for the characterization, classification,
XX differentiation, grading, staging, and/or diagnosis of cell proliferative
XX disorders, or the predisposition to cell proliferative disorders. It can
XX also be used for the therapy of cell proliferative disorders. The present
XX sequence represents a detection oligonucleotide of the invention.
XX
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
```

```
Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1302 TCATATTTTTTTTATTT 1317
Db 3 TGTATTTTTTTTATTT 18

RESULT 999
ADP84381
ID ADP84381 standard; DNA; 20 BP.
XX ADP84381;
XX ADP84381;
XX 23-SEP-2004 (first entry)
XX
XX 5' donor site at the exon 19 splice junction of human AAA1 DNA.
XX
XX ss; AST-1; asthma; IGE mediated disease; human; GPRA;
XX G-protein coupled receptor for asthma susceptibility; AAA1;
XX asthma associated alternatively spliced gene 1;
XX chronic obstructive pulmonary disease; cancer; rhinitis; dermatitis;
XX cystostatic; antiasthmatic; transgenic; asthma locus-1.
XX
XX Homo sapiens.
XX
XX WO2004056866-A1.
XX 08-JUL-2004.
XX 19-DEC-2003; 2003WO-FI000973.
XX
XX 20-DEC-2002; 2002US-0435846P.
XX 03-JAN-2003; 2003US-0437895P.
XX 26-MAR-2003; 2003US-0458767P.
XX 09-JUL-2003; 2003US-0486000P.
XX
XX (GENE-) GENEOS OY.
XX
XX Laitinen T, Kere J, Laitinen LA, Polvi A, Maekela S, Vendelin J;
XX Pulkkinen V, Salmikangas P;
XX WPI; 2004-500286/47.
XX
XX New GPRA polypeptides, useful in preparing a composition for diagnosing,
XX treating or preventing asthma, other IGE-mediated disease, chronic
XX obstructive pulmonary disease or cancer.
XX
XX Example 7; Page 83; 265bp; English.
XX
XX This invention relates to the identification of a novel susceptibility
XX locus AST-1 for asthma and other IGE mediated diseases mapped to the
XX human chromosome 7p14-p15. Specifically, it refers to two overlapping
XX genes namely GPRA (G-protein coupled receptor for asthma susceptibility)
XX and AAA1 (asthma associated alternatively spliced gene 1). The present
XX invention describes identifying single nucleotide polymorphisms, as well
XX as insertion or deletion polymorphisms, occurring at different positions
XX in the AST-1 locus, and furthermore providing vectors, host cells,
XX primers and probes in order to determine the status of an individual.
XX Accordingly, it provides a kit to diagnose or assess predisposition to
XX asthma, chronic obstructive pulmonary disease or cancer and other IGE
XX mediated diseases including rhinitis and dermatitis, such that derived
XX pharmaceutical compositions exhibit cytostatic and antiasthmatic
XX activities. Furthermore, it provides a transgenic animal comprising the
XX asthma locus-1 (AST-1) DNA. This oligonucleotide sequence is a 5' splice
XX junction of the human AAA1 gene, given in Table 11 of the invention.
XX
XX Sequence 20 BP; 12 A; 1 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1515 TAATTAATAAAAAAAAA 1530
 |||||
 Db 5 TAATTAATAATAATAA 20

RESULT 1000
 AAQ68872/c
 ID AAQ68872 standard; DNA; 20 BP.

XX AAQ68872;
 AC
 DT 25-MAR-2003 (revised)
 DT 31-MAR-1995 (first entry)

DE Oligonucleotide (SNA2/ml) used as control in antisense therapy.

XX Oligonucleotide; antisense; self paired; nuclease resistant;
 KM dermatological disorders; viral infection; cancer; atypical dermatitis;
 KM psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
 KM hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
 KM elastase; bone marrow graft; ss.

XX Synthetic.

XX FR2703053-A1.

XX 30-SEP-1994.

XX 26-MAR-1993; 93FR-00003514.

XX 26-MAR-1993; 93FR-00003514.

XX (GEST) GENSET.

XX Vasasseur M, Blumenfeld M, Megueni S, Poddevin B;

XX WPI; 1994-312170/39.

XX New oligonucleotide(s) self paired at one or both ends - have improved
 PT resistance to nuclease(s) and reduced toxicity; useful as anti-sense
 PT molecules for treating dermatological disorders, virus infections,
 PT cancer, etc.

XX Example 1; Fig 4a; 40pp; French.

XX New hooked or semi-hooked oligonucleotides (see AAQ68869-71, AAQ68873,
 CC AAQ68875, AAQ68877, AAQ68879 and AAQ68880) are useful as therapeutic
 CC antisense molecules for treating dermatological disorders (e.g. atypical
 CC dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
 CC (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
 CC directed against an oncogene), due to their ability to hybridise with
 CC target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
 CC grafts. They can also be used for diagnosis or in cosmetics e.g. to block
 CC mRNA coding proteins involved in the ageing process such as collagenase
 CC or elastase. This linear antisense oligonucleotide is used as a control
 CC to see whether the hooked and semi-hooked oligonucleotides exhibit a
 CC greater resistance to exonucleases than linear oligonucleotides. (Updated
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)

XX Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 5.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1302 TCATATTTTATTTT 1317
 |||||
 Db 16 TCATATTTTATTTT 1

RESULT 1001
 AAZ03168/c
 ID AAZ03168 standard; DNA; 20 BP.

XX AAZ03168;

XX 07-OCT-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nongonorrheic trachoma;
 KM paratrachoma; inclusion conjunctivitis; genital disease; perithea;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX Synthetic.

XX Chlamydia trachomatis.

XX W09928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB001939.

XX 28-NOV-1997; 97FR-00015041.

XX 17-DEC-1997; 97FR-00016034.

XX 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.

XX Griffiths R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

XX Disclosure; Page 1584; 1755pp; English.

XX PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nongonorrheic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis, cervicitis, salpingitis, perithea, Bartholinitis;
 CC pneumopathy in breast feeding infants, and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 5.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1182 TGAGCCGATTCGTG 1197
 |||||
 Db 19 TGATGCCGATTCGTG 4

RESULT 1002

AAZ97150
 ID AAZ97150 standard; DNA; 20 BP.

XX AAZ97150;

XX 13-SEP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
OS Synthetic.
OS Chlamydia pneumoniae.
XX
XX MO9927105-A2.
XX
XX PD 03-JUN-1999.
XX
XX PF 20-NOV-1998; 98WO-IB001890.
XX
XX PR 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX
XX PA (GSET) GENSET.
XX
XX PI Griffiths R;
XX DR WPI; 1999-357842/30.
XX
XX PT Genome sequence of Chlamydia pneumoniae.
XX
XX PS Page 1881; Disclosure; 1912p; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae .
XX
SQ Sequence 20 BP; 1 A; 3 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 TTGCTGTCGTCGTCG 740
DB 2 TTGCTGTCGTCGTCG 17

RESULT 1003
AA55806
ID AA55806 standard; DNA; 20 BP.
XX
AC AA55806;
XX
DT 01-SEP-2000 (first entry)
XX
DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:51.
XX
KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200023112-A1.
XX PD 27-APR-2000.
XX PF 19-OCT-1999; 99WO-US024278.
XX PR 19-OCT-1998; 98US-0104804P.

XX
XX PA (METH-) METHYLENE INC.
XX
XX PI Beesterman JM, Macleod AR, Siders WM;
XX
XX DR WPI; 2000-339532/29.
XX
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX of e.g. tumors.
XX
XX PS Disclosure; Page 29; 99p; English.
XX
XX CC The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
XX synergistic amount of an antisense oligonucleotide which inhibits
XX expression of the gene, and an effective synergistic amount of a protein
XX effector of a product of the gene. Also described are: (1) a method for
XX treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX comprising an antisense oligonucleotide which inhibits expression of the
XX gene in operable association with a protein effector of a gene product;
XX and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX methods and compositions are useful as analytical tools for transgenic
XX studies and as therapeutic tools, e.g. as gene therapy tools for human
XX diseases including benign and malignant tumours, inflammation or asthma.
XX The methods, inhibitors and compositions of the invention that inhibit
XX expression or activity of a gene or gene product may be used to treat
XX patients having, or predisposed to developing, a disease responsive to
XX inhibition of the gene. These may also be used to activate silenced genes
XX to provide missing gene functions and improve a given condition.
XX Furthermore, the methods and compositions are useful as probes of the
XX physiological function of a gene product in an experimental cell culture
XX or animal system; and to evaluate the effect of inhibiting gene activity
XX or expression. AA55758 to AA55842 represent oligonucleotide sequences
XX which are used in the exemplification of the present invention
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCCTGTCCTGTCGCC 741
DB 4 TGCCTGTCCTGTCGCC 19

RESULT 1004
AA275633
ID AA275633 standard; DNA; 20 BP.
XX
AC AA275633;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9989.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX


```
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GERT ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8, Page 2360; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 3 A; 7 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1348 ATTTTATTTTCCCTT 1363
Db 1 ATTTATATTTTCCCTT 16
RESULT 1005
ABL57552
XX ABL57552 standard; DNA; 20 BP.
XX
AC ABL57552;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly s.
XX
KM Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
DR WPI; 2000-657765/64.
XX
```

```
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (no
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(s) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1345 TATATTTTATTTTCC 1360
Db 5 TATATTTTATTTTCC 20
RESULT 1006
AAH43116
XX AAH43116 standard; DNA; 20 BP.
XX
AC AAH43116;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-2 121-141.
XX
KM Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; poriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
```

XX Discloure; Page 40; 147pp; English.

XX
XX
CC The sequences given in AAH43115-21 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, reestenosis or pooriasis. They
CC can also be used to treat protozoal and fungal infections

XX
XX Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 726 TGCTGTGCTGCTGCC 741
4 TGCTGCTGCTGCTGCC 19

RESULT 1007
AAC89545
ID AAC89545 standard; DNA; 20 BP.

XX
XX AAC89545;
XX
XX 08-MAR-2001 (first entry)

XX
XX Human HDAC-2 antisense sequence SEQ ID NO: 15.

XX
XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
XX HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
XX gene therapy; PCR primer; ss.

XX
XX Homo sapiens.

XX
XX WO200071703-A2.

XX
XX 30-NOV-2000.

XX
XX 03-MAY-2000; 2000WO-1B001252.

XX
XX 03-MAY-1999; 99US-0132287P.

XX
XX (METH-) METHYLGENE INC.

XX
XX Macleod AR, Li Z, Beesterman JM;
XX WPI; 2001-016407/02.

XX
XX Antisense oligonucleotide that inhibits expression of a histone
XX deacetylase, useful for treating and/or alleviating the symptoms of
XX neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX
XX Example 1; Page 24; 125pp; English.

XX
XX The present invention provides inhibitors of histone deacetylase enzymes
XX such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
XX inhibitors may be antisense strands or they may be compounds identified
XX by contacting the enzyme with the compound and measuring the resulting
XX enzyme activity. These inhibitors are useful for treating cancers and for
XX identifying which histone deacetylase is involved in a neoplasia

XX
XX Sequence 20 BP; 0 A; 7 C; 7 G; 4 T; 2 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.3e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 726 TGCTGTGCTGCTGCC 741
26 TGCTGTGCTGCTGCC 741

Db :|||||
4 UGCTGCTGCTGCTGCC 19

RESULT 1008
AAC89536
ID AAC89536 standard; DNA; 20 BP.

XX
XX AAC89536;
XX
XX 08-MAR-2001 (first entry)

XX
XX Human HDAC-2 PCR primer SEQ ID NO: 6.

XX
XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
XX HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
XX gene therapy; PCR primer; ss.

XX
XX Homo sapiens.

XX
XX WO200071703-A2.

XX
XX 30-NOV-2000.

XX
XX 03-MAY-2000; 2000WO-1B001252.

XX
XX 03-MAY-1999; 99US-0132287P.

XX
XX (METH-) METHYLGENE INC.

XX
XX Macleod AR, Li Z, Beesterman JM;
XX WPI; 2001-016407/02.

XX
XX Antisense oligonucleotide that inhibits expression of a histone
XX deacetylase, useful for treating and/or alleviating the symptoms of
XX neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX
XX Discloure; Page 12; 125pp; English.

XX
XX The present invention provides inhibitors of histone deacetylase enzymes
XX such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
XX inhibitors may be antisense strands or they may be compounds identified
XX by contacting the enzyme with the compound and measuring the resulting
XX enzyme activity. These inhibitors are useful for treating cancers and for
XX identifying which histone deacetylase is involved in a neoplasia

XX
XX Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 726 TGCTGTGCTGCTGCC 741
4 TGCTGCTGCTGCTGCC 19

RESULT 1009
AAH91976/C
ID AAH91976 standard; DNA; 20 BP.

XX
XX AAH91976;
XX
XX 09-OCT-2001 (first entry)

XX
XX Human inflammatory bowel disease associated polymorphic site #1051.

XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.

XX
XX Homo sapiens.

```

XX Key Location/Qualifiers
FH 11
FT misc_feature 11
FT /*tag= a
FT /note= "TA repeat at this position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (ELIIR-) ELIIRISIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K,
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 84; 463bp; English.
XX
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
XX Sequence 20 BP; 10 A; 3 C; 2 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 88.2%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1311 TTTATTTTCAGACAG 1327
XX |||||
XX Db 20 TTTATTTTCAGACAG 4
XX
XX RESULT 1010
XX AAC82913/C
XX ID AAC82913 standard; DNA; 20 BP.
XX
XX AAC82913;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human beta-actin derived oligonucleotide #6.
XX
XX Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
XX
XX DE19923966-A1.
XX
XX 30-NOV-2000.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX

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PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
XX WPI; 2001-050938/07.
XX
XX Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8bp; German.
XX
XX This invention describes a novel recognition system comprising at least 1
XX recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1516 AATTAAAAA 1531
XX |||||
XX Db 17 ACTTAAAAA 2
XX
XX RESULT 1011
XX AAS05714
XX ID AAS05714 standard; DNA; 20 BP.
XX
XX AAS05714;
XX
XX 09-SEP-2004 (revised)
XX
XX 07-SEP-2001 (first entry)
XX
XX Aminopurine substituted region of an RP-TRO.
XX
XX reverse phase triplex forming oligonucleotide; RP-TRO;
XX protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
XX SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX 1 /*tag= a
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX 3 /*tag= b
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX 5 /*tag= c
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX 7 /*tag= d
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX 9 /*tag= e
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX 11 /*tag= f
XX /mod_base= OTHER
XX

```



```
XX      WO2003026566-A2.
PN
XX      03-APR-2003.
PD
XX
XX      13-SEP-2002; 2002WO-US029165.
PF
XX      21-SEP-2001; 2001US-0333997P.
PR
XX      12-SEP-2002; 2002US-00242008.
PR
XX      (UNMI ) UNIV MICHIGAN.
PA
XX      Fink JK, Zhao X;
PI
XX      WPI; 2003-371871/35.
DR
XX      New atlastin gene, useful for preparing a composition for treating
PT      Hereditary Spastic Paraplegia (HSP) or for identifying subjects who have,
PT      or at risk of developing, HSP.
XX
XX      Example 6; Page 102; 11pp; English.
XX
CC      The present invention describes human atlastin, which is located to
CC      chromosome 14 (more specifically to 14q22.1). Also described: (1) an
CC      isolated atlastin polypeptide; (2) identifying subjects who have, or are
CC      at risk of developing, hereditary spastic paraplegia (HSP); (3) a kit for
CC      determining if a subject has, or at risk of developing, HSP; (4) a
CC      computer readable medium encoding a representation of the atlastin
CC      nucleic acid sequence or polypeptide; (6) identifying subjects at risk of
CC      carrying an allele for HSP; and (7) treating a patient with HSP. Atlastin
CC      has neuroprotective activity and can be used in gene therapy. The
CC      atlastin nucleic acid is useful for preparing a composition for treating
CC      HSP or for identifying subjects who have, or at risk of developing, HSP.
CC      The present sequence represents an atlastin intronic splice site
CC      oligonucleotide, which is given in an example from the present invention
XX
XX      Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;
SQ
XX
Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1523 AAAAAAAAAAGTAAAG 1538
      |||||
Dd      18 AAAAAAAAAAGAAAAG 3
RESULT 1014
ABZ86068
ID      ABZ86068 standard; DNA; 20 BP.
XX
AC      ABZ86068;
XX
DT      17-OCT-2003 (first entry)
XX
DE      Human oligonucleotide sequence.
XX
XX      Human; antisense; lung dysfunction; nasal airway dysfunction;
KW      antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW      antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW      antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW      lung inflammation; respiratory disease; ds.
XX
OS      Homo sapiens.
XX
PN      WO200285308-A2.
XX
PD      31-OCT-2002.
XX
PF      23-APR-2002; 2002WO-US013135.
PR      24-APR-2001; 2001US-0286137P.
```

```
XX      (EPiG-) EPIGENESIS PHARM INC.
PA
XX      Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI      Miller S, Tang L, Shahbuddin S;
XX
XX      WPI; 2003-229219/22.
DR
XX
XX      Pharmaceutical composition for treating ailments associated with impaired
PT      respiration, has oligo(s) antisense to specific gene(s) or its
PT      corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT      ubiquinone.
XX
XX      Claim 15; SEQ ID NO 1310; 872pp; English.
XX
XX      The invention relates to a novel pharmaceutical composition, which has a
CC      first active agent comprising an oligonucleotide antisense to the
CC      initiation codon, coding region, 5' or 3' end, genomic flanking regions,
CC      5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC      junctions of genes encoding a polypeptide associated with lung and/or
CC      nasal airway dysfunction and a second active agent comprising an
CC      antiinflammatory steroid and ubiquinone. A composition of the invention
CC      has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC      immunosuppressive, and cytosstatic activity. The composition may have a
CC      use in antisense gene therapy. The composition is useful for treating or
CC      preventing a respiratory, lung or malignant disease or condition, also
CC      for enhancing the prophylactic or therapeutic respiratory effect of an
CC      antiinflammatory steroid in a subject, for reducing or depleting levels
CC      of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC      receptor, producing bronchodilation, increasing levels of ubiquinone or
CC      lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC      lung inflammation, lung allergies, or a respiratory disease or condition.
CC      Note: The sequence data for this patent is not represented in the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
XX
Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      726 TGCTGTTGCTGCTGCC 741
      |||||
Dd      4 TGCTGCTGCTGCTGCC 19
RESULT 1015
ABZ87682
ID      ABZ87682 standard; DNA; 20 BP.
XX
AC      ABZ87682;
XX
DT      17-OCT-2003 (first entry)
XX
DE      Human oligonucleotide sequence.
XX
XX      Human; antisense; lung dysfunction; nasal airway dysfunction;
KW      antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW      antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW      antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW      lung inflammation; respiratory disease; ds.
XX
OS      Homo sapiens.
XX
PN      WO200285308-A2.
XX
PD      31-OCT-2002.
XX
PF      23-APR-2002; 2002WO-US013135.
PR      24-APR-2001; 2001US-0286137P.
```

```
XX XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 2924; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1306 TTTTATTATTTTCAG 1321
DB 1 TTTTATTTTTCAG 16
XX
RESULT 1016
AB288879
ID AB288879 standard; DNA; 20 BP.
XX
AC AB288879;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
```

```
XX XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 4121; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 1 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1516 AATTAAAAA 1531
DB 4 ACTTAAAAA 19
XX
RESULT 1017
AB297707/C
ID AB297707 standard; DNA; 20 BP.
XX
AC AB297707;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human CCR3 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
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XX (EPiG-) EPIGENESIS PHARM INC.
PA
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
DR
XX Pharmacological composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqtuone.
XX
XX PS Disclosure; SEQ ID NO 12949; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqtuone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqtuone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1524 AAAAAAAAAAGTCAAG 1539
XX |||||
XX Db 17 AAAAAAAAAAGTCAAG 2
XX
XX RESULT 1018
XX AB291518 standard; DNA; 20 BP.
XX
XX AC AB291518;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqtuone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
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XX (EPiG-) EPIGENESIS PHARM INC.
PA
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
DR
XX Pharmacological composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqtuone.
XX
XX PS Disclosure; SEQ ID NO 6760; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqtuone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqtuone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 666 GACTCACCTCTGACGC 681
XX |||||
XX Db 1 GACTCACCTCTGTCGC 16
XX
XX RESULT 1019
XX AB289678 standard; DNA; 20 BP.
XX
XX AC AB289678;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqtuone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
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XX (FIG-) EPIGENESIS PHARM INC.
PA
XX Nye JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4920; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cyostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1521 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 17
XX
RESULT 1020
ABZ93536
ID ABZ93536 standard; DNA; 20 BP.
XX
AC ABZ93536;
XX
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
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XX (FIG-) EPIGENESIS PHARM INC.
PA
XX Nye JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8778; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cyostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1295 TGGTTAATCTATTTT 1310
DB 1 TGGTTAATCTTTT 16
XX
RESULT 1021
ABZ88813
ID ABZ88813 standard; DNA; 20 BP.
XX
AC ABZ88813;
XX
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
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PA (BFIG-1) EPIDEMIOLOGIS PHARM INC.
XX
XX NYCE JW, Li Y, Sandraeagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquitinone.
XX
PS Disclosure; SEQ ID NO 4055; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' and genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquitinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquitinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1516 AATTAAAAA 1531
||| |||||
Db 2 AATTAAAAA 17

RESULT 1022
AB286072
ID AB286072 standard; DNA; 20 BP.
XX
AC AB286072;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquitinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.

XX	(EPiG-) EPIGENESIS PHARM INC.
PA	
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pablan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	WP1; 2003-229219/22.
DR	
XX	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(e)s antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquone.
PS	
XX	Claim 15; SEQ ID NO 1314; 872bp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end, genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytosstatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
SQ	
Sequence	20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity	93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	
726 TGCTGTGTCGTGCC 741	
1 TGCTGTGTCGTGCC 16	
Db	
RESULT 1023	
ABD22298	
ID ABD22298 standard; DNA; 20 BP.	
AC	
ABD22298;	
D7	
29-JUL-2004 (first entry)	
DE	
Human stannocalcin-derived oligo SEQ ID 1310.	
XX	
Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
KW	respiratory tract inflammation; adenoma sensitivity; lung; cancer;
KW	suffactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW	analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;
KW	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW	pulmonary transplantation rejection; ss; primer.
OS	
Homo sapiens.	
XX	
WO200285309-A2.	
PN	
31-OCT-2002.	
DD	
23-APR-2002; 2002WO-USO13143.	
PF	

ID ABD29766 standard; DNA; 20 BP.
XX
AC ABD29766;
XX
DT 29-JUL-2004 (first entry)
XX
DE R37953-derived oligonucleotide SEQ ID 8778.
XX
KM Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 8778; 763bp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1295 TGGTTAATCTTTT 1310
DB 1 TGGTTAATCTTTT 16
XX
RESULT 1026
ID ABD23912 standard; DNA; 20 BP.
XX
AC ABD23912;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human calmodulin 2-derived oligonucleotide SEQ ID 2924.
XX
KM Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 2924; 763bp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated

CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	diseases syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
SQ	Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;
	Query Match 1.0%; Score 14.4; DB 1; Length 20;
	Best Local Similarity 93.8%; Pred. No. 5.3e+02;
	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy	1306 TTTTATTTTCAG 1321 1 TTTTTTTTTTCAG 16
Dd	
RESULT 1027	
ID	ABD30738/C
XX	ABD30738 standard; DNA; 20 BP.
AC	
XX	ABD30738;
DT	
XX	29-JUL-2004 (first entry)
DS	
XX	Human CCR3-derived oligonucleotide SEQ ID 12949.
KW	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW	respiratory tract inflammation; adenosis sensitivity; lung; cancer;
KW	antifungal depletion; antiallergic; anti-inflammatory; antiasthmatic;
KM	analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KM	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW	pulmonary transplantation rejection; ss; primer.
XX	
OS	Homo sapiens.
XX	
PN	WO200285309-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002MO-US013143.
XX	
PR	24-APR-2001; 2001US-0286036P.
XX	
PA	(EPIC-) EPIGENESIS PHARM INC.
XX	
P1	Nyce JM, Li Y, Sandrasegria A, Katz E, Pabalan J, Aguilar D;
P1	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
FT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
XX	
PS	Claim 15; SEQ ID NO 12949; 763BP; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	succinate depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device; in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability, or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or surfactant hypoproduction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
SQ	Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
Query Match	1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity	93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Cy	1524 AAAAAAAAAGTTAAAG 1539 17 AAAAAAAGTCAACAG 2
Db	
RESULT 1028	
ABD25109	
ID ABD25109 standard; DNA; 20 BP.	
XX AC	
XX ABD25109;	
DT 29-JUL-2004 (first entry)	
XX	
DE All25228-derived oligonucleotide SEQ ID 4121.	
XX DS	
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
KW respiratory tract inflammation; adenovirus sensitivity; lung; cancer;	
KW surfactant depletion; anti-allergic; anti-inflammation; antiasthmatic;	
KW analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;	
KW beta-adrenergic antagonist; respiratory disease; pulmonary vasoconstriction;	
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;	
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;	
KW pulmonary transplantation rejection; ss; primer.	
XX	
OS Homo sapiens.	
XX	
PN WO200285309-A2.	
XX	
PD 31-OCT-2002.	
XX	
PF 23-APR-2002; 2002WO-USO13143.	
XX	
PR 24-APR-2001; 2001US-0286036P.	
XX	
PA (BPIG-) EPIGENESIS PHARM INC.	
XX	
P1 Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
P1 Miller S, Tang L, Shahbuddin S;	
XX	
DR WPI; 2003-093056/08.	
XX	
PT Pharmaceutical composition for treating asthma, has antisense	
PT oligonucleotide containing less percentage of adenosine, targeted to	
PT nucleic acids associated with lung airway or lung dysfunction, and	

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
FN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PP 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15, SEQ ID NO 6760; 763bp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity. Levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, anti-asthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperinflation, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 666 GACTCAGCTGTAGCG 681
|||
Db 1 GACTCAGCTGTCTCC 16

RESULT 1031
ADJ59564/C
ID ADJ59564 standard; DNA; 20 BP.

XX
AC ADJ59564;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to CCR3 #65.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
FN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PP 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Tang L, Sandrasegura A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
CC Novel single or multiple target oligonucleotide anti-sense to e.g.
CC initiation codons and introns of respiratory disease-relevant genes e.g.,
CC CCR3, RANTES, MCP4, useful for prophylaxis or treating respiratory
CC disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 420; 85bp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotide of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or sales of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1524 AAAAAGTAAGG 1539
|||
Db 17 AAAAAGTAAGG 2

RESULT 1032
ADK80880/C
ID ADK80880 standard; DNA; 20 BP.

XX
AC ADK80880;
XX
DT 20-MAY-2004 (first entry)
XX


```
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8214.
XX Nav1.3; Analgesic; Noctropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
OS Synthetic.
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL,
XX
XX WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX
XX Claim 4; SEQ ID NO 8214; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy, or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a decoy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 11 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query March 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1252 TTTTGTTTTAAATCA 1267
Db 17 TTTTGATTTTAAATCA 2
RESULT 1033
ADO45054/C
ID ADO45054 standard; DNA; 20 BP.
XX
AC ADO45054;
XX
XX 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #420.
XX
KM Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KM CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICM; VCM; tryptase a;
KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KM lung disease; hyper-responsiveness; adenosine and/or levels of adenosine A
KM asthma; lung allergy; inflammation; inflammatory disease;
KM asthma; inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KM acute respiratory distress syndrome; pulmonary hypertension;
```

```
KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
XX Homo sapiens.
XX
XX US2004049022-A1.
XX
XX 11-MAR-2004.
XX
XX 25-JUL-2003; 2003US-00627930.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
XX
XX (SAND/) SANDRASAGRA A.
XX
XX (TANG/) TANG L.
XX
XX (AGUI/) AGUIAR D.
XX
XX (MILL/) MILLER S.
XX
XX (SHAH/) SHAHABUDDIN S.
XX
XX (LUHH/) LU H.
XX
XX (CONG/) CONG H.
XX
XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-293804/27.
XX
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
XX asthma.
XX
XX Claim 2; SEQ ID NO 420; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICM, VCM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICM, VCM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
Query March 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1524 AAAAAAAAAAAGG 1539
Db 17 AAAAAAAAAAGTCAAGG 2
RESULT 1034
ADO55869/C
ID ADO55869 standard; DNA; 20 BP.
```

```
XX AC ADO55869;
XX XX 12-AUG-2004 (first entry)
XX DE Human NIMA-related kinase 6 DNA target sequence #23.
XX XX
XX XX Antisense therapy; human; NIMA-related kinase 6;
XX KW never in mitosis gene a-related kinase 6; hyperproliferative disorder;
XX KW cancer; cytosstatic; ds.
XX OS Homo sapiens.
XX XX
XX XX US2004097441-A1.
XX PD 20-MAY-2004.
XX PF 16-NOV-2002; 2002US-00295471.
XX PR 16-NOV-2002; 2002US-00295471.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dobie KW;
XX DR WPI; 2004-389184/36.
XX PT New antisense oligonucleotides for modulating never in mitosis, gene a
XX PT (NIMA)-related kinase 6 expression, useful for diagnosing, preventing or
XX PT treating diseases associated with the kinase, e.g. hyperproliferative
XX PT disorders.
XX PS Example 15; SEQ ID NO 115; 51bp; English.
XX XX
XX CC The present invention relates to antisense compounds targeted to a
XX CC nucleic acid encoding human never in mitosis gene a-related kinase 6
XX CC (NIMA-related kinase 6). The antisense compound comprises an antisense
XX CC oligonucleotide that specifically hybridizes with the nucleic acid and
XX CC inhibits the expression of NIMA-related kinase 6. The antisense
XX CC oligonucleotide is a chimeric oligonucleotide. The antisense
XX CC oligonucleotide comprises at least one modified internucleoside linkage,
XX CC preferably a phosphorothioate linkage. It also comprises at least one
XX CC modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
XX CC moiety. The antisense oligonucleotide further comprises at least one
XX CC modified nucleobase, preferably a 5-methylcytosine. The antisense
XX CC oligonucleotides are useful for the treatment of diseases such as
XX CC hyperproliferative disorders, e.g. cancer. The present sequence
XX CC represents a human NIMA-related kinase 6 DNA target sequence for an
XX CC antisense oligonucleotide.
XX SQ Sequence 20 BP; 5 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1036 AGTGGCGCGCGGTGCT 1051
DB 20 AGTGGCGTCCGCTGCT 5
RESULT 1035
ADP055807 standard; DNA; 20 BP.
AC ADO55807;
XX XX
XX XX 12-AUG-2004 (first entry)
XX DE Human NIMA-related kinase 6 DNA, antisense oligonucleotide #30.
XX XX
XX KW Antisense therapy; human; NIMA-related kinase 6;
XX KW never in mitosis gene a-related kinase 6; hyperproliferative disorder;
```

```
KW KW cancer; cytosstatic; phosphorothioate; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "This oligonucleotide has a phosphorothioate
XX FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
XX FT and 3' ends, which are 5 nucleotides in length at each
XX FT end. All cytidine residues are 5-methylcytidines"
XX FT
XX PN US2004097441-A1.
XX PD 20-MAY-2004.
XX PF 16-NOV-2002; 2002US-00295471.
XX PR 16-NOV-2002; 2002US-00295471.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dobie KW;
XX DR WPI; 2004-389184/36.
XX PT New antisense oligonucleotides for modulating never in mitosis, gene a
XX PT (NIMA)-related kinase 6 expression, useful for diagnosing, preventing or
XX PT treating diseases associated with the kinase, e.g. hyperproliferative
XX PT disorders.
XX PS Example 15; SEQ ID NO 44; 51bp; English.
XX XX
XX CC The present invention relates to antisense compounds targeted to a
XX CC nucleic acid encoding human never in mitosis gene a-related kinase 6
XX CC (NIMA-related kinase 6). The antisense compound comprises an antisense
XX CC oligonucleotide that specifically hybridizes with the nucleic acid and
XX CC inhibits the expression of NIMA-related kinase 6. The antisense
XX CC oligonucleotide is a chimeric oligonucleotide. The antisense
XX CC oligonucleotide comprises at least one modified internucleoside linkage,
XX CC preferably a phosphorothioate linkage. It also comprises at least one
XX CC modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
XX CC moiety. The antisense oligonucleotide further comprises at least one
XX CC modified nucleobase, preferably a 5-methylcytosine. The antisense
XX CC oligonucleotides are useful for the treatment of diseases such as
XX CC hyperproliferative disorders, e.g. cancer. The present sequence
XX CC represents an antisense oligonucleotide used in the examples of the
XX CC present invention.
XX SQ Sequence 20 BP; 2 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1036 AGTGGCGCGCGGTGCT 1051
DB 1 AGTGGCGTCCGCTGCT 16
RESULT 1036
ADP20520/C standard; DNA; 20 BP.
AC ADP20520;
XX XX
XX XX 26-AUG-2004 (first entry)
XX DE Transcription factor AP-2 antisense oligonucleotide seqid 67.
XX XX
XX KW Cytostatic; AP-2-inhibitor-Alpha; AP-2 alpha; AP-2 alpha modulator;
XX KW AP-2 alpha associated disorder; hyperproliferative disorder; human;
```

KM transcription factor; antisense oligonucleotide; antisense technology;
KM ss.
XX Homo sapiens.
OS
XX US2004109648-A1.
PN
XX 10-JUN-2004.
PD
XX 09-DEC-2002; 2002US-00315962.
PF
XX 09-DEC-2002; 2002US-00315962.
PR
XX (ISIS-) ISIS PHARM INC.
PA
PI Bennett CF, Dean NM, Freier SM, Dobie KM;
XX WPI; 2004-440306/41.
DR
XX
XX
PT New compounds targeted to nucleic acid molecules encoding AP-2 alpha and
PT inhibits the expression of AP-2 alpha, useful for treating AP-2 alpha-
PT associated disease or condition, particularly a hyperproliferative
PT disorder.
XX
XX Example 15; SEQ ID NO 67; 58bp; English.
PS
XX
XX The invention describes a compound (I) 8-80 nucleobases in length
CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
CC (1866 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
CC comprising contacting the cells or tissues with (I); screening for a
CC modulator of AP-2 alpha by contacting a preferred target segment of a
CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
CC alpha expression, which modulate the expression of AP-2 alpha; a
CC diagnostic method for identifying a disease state; and a kit or assay
CC device comprising (I). The compound is useful for treating an animal
CC having a disease or condition associated with AP-2 alpha, particularly a
CC hyperproliferative disorder. The compounds may be used for diagnosis,
CC therapeutics prophylaxis and as research reagents; or as tools in
CC differential and/or combinatorial analyses to elucidate expression
CC patterns of a portion or the entire complement of genes expressed within
CC cells and tissues. This sequence represents a human transcription factor
CC AP-2 antisense oligonucleotide.
XX
XX Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 726 TGGTGTGCTGCTGCTGCC 741
DB 18 TGCTGCTGCTGCTGCTGC 3
RESULT 1037
ADP21858/C
ID ADP21858 standard; DNA; 20 BP.
XX
XX ADP21858;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX Human ornithine decarboxylase 1 primer seqid 6.
DE
XX
XX cytosolic; gene therapy; ornithine decarboxylase 1;
KM ornithine decarboxylase 1 associated disorder;
KM hyperproliferative disorder; cancer; human; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX

PN US2004110148-A1.
XX
XX 10-JUN-2004.
PD
XX 10-DEC-2002; 2002US-00316244.
PF
XX 10-DEC-2002; 2002US-00316244.
PR
XX (ISIS-) ISIS PHARM INC.
PA
PI Bennett CF, Dobie KM;
XX WPI; 2004-440337/41.
DR
XX
XX
PT New oligonucleotide compound that inhibits expression of ornithine
PT decarboxylase 1, useful for preparing a composition for treating
PT hyperproliferative disorder, e.g. cancer.
XX
XX Claim 21; SEQ ID NO 6; 69bp; English.
PS
XX
XX The invention describes a new compound, having a sequence comprising 8-80
CC bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
CC specifically hybridises with the nucleic acid encoding ornithine
CC decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
CC ornithine decarboxylase 1. Also described are: inhibiting the expression
CC of ornithine decarboxylase 1 in cells or tissues; screening for a
CC modulator of ornithine decarboxylase 1; identifying a disease state; a
CC kit or assay device comprising the compound; and treating an animal
CC having a disease or condition associated with ornithine decarboxylase 1.
CC The oligonucleotide compound is useful for preparing a composition for
CC treating hyperproliferative disorder, e.g. cancer. This sequence
CC represents a primer used to isolate DNA encoding human ornithine
CC decarboxylase 1.
XX
XX Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 729 TGGTGTGCTGCTGCTTT 744
DB 20 TGTTGTGCTGCTGCTCT 5
RESULT 1038
AAQ75552
ID AAQ75552 standard; DNA; 19 BP.
XX
XX AAQ75552;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
KM
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) the
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1246 TCTTGTGTTGTTTAA 1264
DB 1 TTTTGTGTTTGTGTTTAA 19
XX
RESULT 1039
ID ADL79331 standard; RNA; 19 BP.
XX
AC ADL79331;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human HER2 (EGFR2) siNA lower strand, SEQ ID NO:496.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
KW HER2; EGFR2; neu; erbB2; C-erb-B-2; ss.
XX
OS Homo sapiens.
XX
PN WO2003070912-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005045.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US016840.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393924P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 19-SEP-2002; 2002US-00251117.
PR 21-OCT-2002; 2002US-00277494.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcawlggen J, Pavco P, Beigelman L, Fossnaugh K, Jamison S;
XX
DR WPI, 2003-697612/66.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX

PS Example 3; SEQ ID NO 496; 171pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of EGFR genes in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the lower strand of a
CC HER2 (EGFR2)-targeted double-stranded siNA.
XX
SQ Sequence 19 BP; 16 A; 2 C; 0 G; 0 T; 1 U; 0 Other;
XX
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 6.1e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1519 TAAAAAAGTAAAA 1537
DB 1 UAAAAACAAAAA 19
XX
RESULT 1040
ID ADL79082/C
XX
ADL79082 standard; RNA; 19 BP.
XX
AC ADL79082;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human HER2 (EGFR2) transcript target sequence/siNA upper strand, SEQ:247.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
KW HER2; EGFR2; neu; erbB2; C-erb-B-2; target sequence; ss.
XX
OS Homo sapiens.
XX
PN WO2003070912-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005045.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US016840.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393924P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 19-SEP-2002; 2002US-00251117.
PR 21-OCT-2002; 2002US-00277494.
XX

PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI McGwigen J, Pavco P, Belgelman L, Fossnaugh K, Jamison S;
XX WPI; 2003-697612/66.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX
PS Example 3; SEQ ID NO 247; 171pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNA may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNA include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNA can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNA are
CC used to modulate expression of EGFR genes in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC siNA are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the upper strand of a
CC human HER2 (EGFR2)-targeted double-stranded siNA, which is identical to
CC the HER2 transcript target sequence.
XX
XX Sequence 19 BP; 1 A; 0 C; 2 G; 0 T; 16 U; 0 Other;
SQ

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAA 1537
|||
Dd 19 TAAAAACAAAACAAA 1

RESULT 1041
AB269546/c
ID AB269546 standard; DNA; 20 BP.
XX
AC AB269546;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX PN W0200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
PP

XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4788; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
SQ

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1246 TCTTGTGTTTAAAA 1264
|||
Dd 19 TTTTGTGTTTAAAA 1

RESULT 1042
ABD25776/c
ID ABD25776 standard; DNA; 20 BP.
XX
AC ABD25776;
XX
DT 29-JUL-2004 (first entry)
XX
DE A1085559 DNA fragment.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX OS
XX PN W0200285309-A2.
XX
XX PD 31-OCT-2002.
XX

XX	23-APR-2002; 2002MO-US0313143.
PF	
XX	24-APR-2001; 2001US-0286036P.
PR	
XX	
XX	(EPIC-) EPIGENESIS PHARM INC.
XX	
PI	Nyge JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shanabuddin S;
XX	
DR	WPI; 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
XX	
XX	Claim 15; SEQ ID NO 4788; 763bp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	surfactant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has antiallergic, antiinflammatory, antispasmodic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability, or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	dysregulation, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
XX	Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
SQ	
	Query Match 1.0%; Score 14.2; DB 1; Length 20;
	Best Local Similarity 84.2%; Pred. No. 5.8e-02;
	Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
OY	1246 TCTTGTGTTGTTTAA 1264
Db	19 TTTTTTTTTTTTTTAA 1
RESULT 1043	
AA075579	
ID	AA075579 standard; DNA; 20 BP.
XX	
XX	AA075579;
XX	
XX	04-AUG-1995 (first entry)
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
XX	Analysis, gene expression; reverse transcription; primer; cDNA;
XX	aggregate; restriction enzyme; ss.
XX	

```

XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PE 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
Cy 1246 TCCTTGTTTGTTTAA 1264
Db 1 TTTT TTTT TTTT TTTTAA 19
RESULT 1044
AAQ75582
ID AAQ75582 standard; DNA; 20 BP.
AC
AC AAQ75582;
XX
DT 04-AUG-1995 (first entry)
XX
DB Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX PN
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 TCTTTGTTTGTGTTTTTAA 1264
1 TTTTGTGTTTGTGTTTTTAA 19
Db 1 TTTTGTGTTTGTGTTTTTAA 19
RESULT 1045
AAQ75580
ID AAQ75580 standard; DNA; 20 BP.
XX
AC AAQ75580;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 TCTTTGTTTGTGTTTTTAA 1264
1 TTTTGTGTTTGTGTTTTTAA 19
Db 1 TTTTGTGTTTGTGTTTTTAA 19
RESULT 1046
ABZ88694/c
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ID ABZ88694 standard; DNA; 20 BP.
XX
AC ABZ88694;
XX
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KM Human; antitense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antitense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antitense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3936; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antitense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antitense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 TCTTTGTTTGTGTTTTTAA 1264
20 TTTTGTGTTTGTGTTTTTAA 2
Db 20 TTTTGTGTTTGTGTTTTTAA 2
RESULT 1047
AAQ75596
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ID AAQ75596 standard; DNA; 20 BP.
XX
XX AAQ75596;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX MPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 5.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1302 TCTATTTTTTTTATTTCA 1320
XX | | | | | | | | | |
XX 1 TTTTTTTTTTTTTTTCA 19
XX
XX RESULT 1048
XX AAQ75597
XX ID AAQ75597 standard; DNA; 20 BP.
XX
XX AAQ75597;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX MPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 5.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1302 TCTATTTTTTTTATTTCA 1320
XX | | | | | | | | | |
XX 1 TTTTTTTTTTTTTTTCA 19
XX
XX RESULT 1049
XX AAQ75595/c
XX ID AAQ75595 standard; DNA; 20 BP.
XX
XX AAQ75595;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX MPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX

```

Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1518 TTTAAAAAAAGTAA 1536
19 TTTAAAAAAAGTAA 1

RESULT 1050

AB285312

ID AB285312 standard; DNA; 20 BP.

AC AB285312;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

Human; antisease; lung dysfunction; nasal airway dysfunction;
antiflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiallergic; hypotensive; immunosuppressive; cyostatic; gene therapy;
antisease gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisease to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

Claim 15; SEQ ID NO 554; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisease to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiallergic, hypotensive,
immunosuppressive, and cyostatic activity. The composition may have a
use in antisease gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1302 TCTATTTTATTTTCA 1320
2 TTTTATTTTATTTTCA 20

RESULT 1051

ABD21542

ID ABD21542 standard; DNA; 20 BP.

AC ABD21542;

DT 29-JUL-2004 (first entry)

DE 5100 calcium binding protein A2-derived oligo SEQ ID 554.

Human; antisease; bronchoconstriction; allergy; hyposecretion; pain;
respiratory tract inflammation; adenosine sensitivity; lung; cancer;
surfactant depletion; antiallergic; antiinflammatory; antiallergic;
analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;
beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
pulmonary transplantation rejection; ss; primer.

Homo sapiens.

WO200285309-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-) EPIGENESIS PHARM INC.

NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisease
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and
bronchodilating agent.

Claim 15; SEQ ID NO 554; 763pp; English.

This invention describes a novel composition (a) a first active agent,
comprising oligonucleotides, effective for alleviating
bronchoconstriction, respiratory tract inflammation, allergies and
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
surfactant depletion or hyposecretion, when administered to a mammal. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and can be anti-sense to the corresponding mRNA.
The invention also describes a kit, that comprises: (a) a delivery
device, in separate containers, (b) the oligonucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has antiallergic, antiinflammatory, antiallergic,
analgesic, hypotensive, immunosuppressive and cyostatic activity, is a
beta-adrenergic agonist. The composition is useful for preventing or
treating a respiratory, lung or malignant disease. The administered
composition comprises oligo and is administered to reduce the production
or availability, or to increase the degradation of the target mRNA or to
reduce the amount of target polypeptide present in the lungs. The
pulmonary obstruction, and/or bronchoconstriction and/or lung
inflammation, allergies and/or surfactant hypoproduction are associated
with a disease or condition such as pulmonary vasoconstriction,
inflammation, allergies, asthma, impeded respiration, respiratory

CC diarrhoea syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperaemia, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SO Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1302 TCTATTTTATTTTATTTCA 1320

DB 2 TTTTATTTTATTTTATTTCA 20

RESULT 1052

AAQ75586 ID AAQ75586 standard; DNA; 20 BP.

XX AAQ75586;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis: gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

SO Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1248 TTGCTTTTGTTTTATTC 1266

DB 2 TTTTATTTTATTTTATTC 20

RESULT 1053

AAQ75576 ID AAQ75576 standard; DNA; 20 BP.

XX AAQ75576;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis: gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

SO Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1304 TATTTTATTTTATTTTCA 1322

DB 2 TTTTATTTTATTTTATTTCA 20

RESULT 1054

AAQ68872 ID AAQ68872 standard; DNA; 20 BP.

XX AAQ68872;

XX 25-MAR-2003 (revised)

DT 31-MAY-1995 (first entry)

DE Oligonucleotide (SA12/ml) used as control in antisense therapy.

XX Oligonucleotide; antisense; self paired; nuclease resistant;
KW dermatological disorders; viral infection; cancer; atypical dermatitis;
KW psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KW hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KW elastase; bone marrow graft; ss.

OS Synthetic.

PN FR2703053-A1.

PD 30-SEP-1994.

```

XX 26-MAR-1993; 93FR-00003514.
PF
XX
PR 26-MAR-1993; 93FR-00003514.
XX
PA (GEST ) GENSET.
XX
PI Vasseur M, Blumenfeld M, Meguenni S, Poddevyn B;
DR WPI; 1994-312170/39.
XX
PT New oligo:nucleotide(s) self paired at one or both ends - have improved
PT resistance to nuclease(s) and reduced toxicity, useful as anti:sense
PT molecules for treating dermatological disorders, virus infections,
PT cancer, etc.
XX
PS Example 1; Fig 4a; 40pp; French.
XX
CC New hooked or semi-hooked oligonucleotides (see AA068869-71, AA068873,
CC AA068875, AA068877, AA068879 and AA068880) are useful as therapeutic
CC antisense molecules for treating dermatological disorders (e.g. atypical
CC dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
CC (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
CC directed against an oncogene), due to their ability to hybridise with
CC target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
CC grafts. They can also be used for diagnosis or in cosmetics e.g. to block
CC mRNA coding proteins involved in the ageing process such as collagenase
CC or elastase. This linear antisense oligonucleotide is used as a control
CC to see whether the hooked and semi-hooked oligonucleotides exhibit a
CC greater resistance to exonucleases than linear oligonucleotides. (Updated
CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other:

```

```

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 1520 AAAAAAAAAAAGTAAAG 1538
Db 1 AAAAAAAAAAATGAAAG 19

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RESULT 1055
ACF57337
ID ACF57337 standard; DNA; 20 BP.
XX
AC ACF57337;
XX
DT 16-OCT-2003 (first entry)
XX
DE Human atlastin exon 10 intronic acceptor splice site.
XX
KW Human; atlastin; chromosome 14; 14q22.1; hereditary spastic paraplegia;
KW HSP; neuroprotective; gene therapy; intronic splice site; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003026566-A2.
XX
PD 03-APR-2003.
XX
PF 13-SEP-2002; 2002WO-US029165.
XX
PR 21-SEP-2001; 2001US-0323997P.
PR 12-SEP-2002; 2002US-00242008.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Fink JK, Zhao X;
XX

```

```

DR WPI; 2003-371871/35.
XX
PT New atlastin gene, useful for preparing a composition for treating
PT Hereditary Spastic Paraplegia (HSP) or for identifying subjects who have,
PT or at risk of developing, HSP.
XX
PS Example 6; Page 102; 11pp; English.
XX

```

```

CC The present invention describes human atlastin, which is located to
CC chromosome 14 (more specifically to 14q22.1). Also described: (1) an
CC isolated atlastin polypeptide; (2) identifying subjects who have, or are
CC at risk of developing, hereditary spastic paraplegia (HSP); (3) a kit for
CC determining if a subject has, or at risk of developing, HSP; (4) a
CC computer readable medium encoding a representation of the atlastin
CC nucleic acid sequence or polypeptide; (6) identifying subjects at risk of
CC carrying an allele for HSP; and (7) treating a patient with HSP. Atlastin
CC has neuroprotective activity and can be used in gene therapy. The
CC atlastin nucleic acid is useful for preparing a composition for treating
CC HSP or for identifying subjects who have, or at risk of developing, HSP.
CC The present sequence represents an atlastin intronic splice site
CC oligonucleotide, which is given in an example from the present invention
XX
SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other:

```

```

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1245 ATCTTGTTCCTTTTGA 1263
Db 1 ATCTTTCCTTTTTCCTTTTGA 19

```

```

Search completed: November 2, 2004, 12:44:19
Job time : 22 secs

```


was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473114[g1473114]Af129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1515 TAATTAATAAAAAAAAAAAGTAAAA 1537
Db 1 TATTTAAAAAATAAAAAAAAAAAAAA 23

RESULT 5
TA231E08Q 22 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 231e08, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL480935.1 GI:11846704
VERSION AL480935.1 GI:11846704
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
JOURNAL project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
SOURCE location/Qualifiers

1. 22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strains="TREU927"
/db_xref="taxon:5691"
/clone="231e08"

Query Match 1.3%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAGCG 1540
Db 1 AAAAAAAAAAAGCG 21

RESULT 6
AJ663467 25 bp mRNA linear EST 28-JUN-2004
LOCUS AJ663467 CSEBRAN09 Sus scrofa cDNA clone C000027_007, mRNA
DEFINITION sequence.

ACCESSION AJ663467.1 GI:49347590
VERSION AJ663467.1
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

AUTHORS 1 (bases 1 to 25)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)

JOURNAL Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -mnscore 20
and -mismatch 12 options. Vector: pluescriptII (KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
SOURCE location/Qualifiers

1. 25
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000027_007"
/tissue_type="placenta"
/clone_lib="CSEBRAN09"
/note="Vector: pluescriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 1.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAGCG 1540
Db 3 AAAAAAAAAAAGCG 23

RESULT 7
CF291636 24 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-C09, mRNA
sequence.

ACCESSION CF291636.1 GI:33660669
VERSION CF291636
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

Source

1. 24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-C09"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 424 GTGGCGCTGCGCGCGCGCGCGCG 447
|||||
Db 1 GCGCGCGCGCGCGCGCGCGCGCG 24

RESULT 8
A2309553 24 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0016B10F Mouse 10kb plasmid UUCGIM library Mus musculus genomic
DEFINITION clone UUCGIM0016B10 F, genomic survey sequence.
ACCESSION A2309553
VERSION A2309553.1 GI:10350837
KEYWORDS GSS.
ORGANISM Mus musculus (house mouse)
SOURCE Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: B column: 10
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

Source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGIM0016B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g1473214[g1473214]p129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1514 TTAATTAAATAAAAGTAAA 1537
|||||
Db 1 TTTTAAAAAAAAAAAAAAAA 24

RESULT 9
CF317007/c 25 bp mRNA linear EST 15-AUG-2003
LOCUS HD--06-114.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-114, mRNA sequence.
ACCESSION CF317007
VERSION CF317007.1 GI:33688768
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiales; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 25)
Kim, J.-S., Yun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K., and Nahm, B.-H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

Source

1. 25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1514 TTAATTAATAAAAAAAAAAGTAAAA 1537
 DB 25 TTTAAAAAAAAAAAAAAAAAAAAA 2

RESULT 10
 LOCUS T49097/c
 DEFINITION yb08h08.g1 Stragene placenta (#937225) Homo sapiens cDNA clone IMAGE:70623.3, similar to gb:K6724 CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097
 VERSION T49097.1
 KEYWORDS GI:650957
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisage, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thiertry-Weg, J., Trevaakie, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 PUBMED 8889549
 COMMENT Other ESTs: yb08h08.r1
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNLN.
 This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21m3
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:491520"
 /db_xref="taxon:9606"
 /clone="IMAGE:70623"
 /sex="male"
 /lab_host="SOUR cells (kanamycin resistant)"
 /clone_1lb="Stragene placenta (#937225)"
 /note="Organ: placenta; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAAATCGGACGAG 3' -3' adaptor sequence: 5' CTCGAGCTTTTCTTTTCTTTT 3'."

Query Match 1.3%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1514 TTAATTAATAAAAAAAAAAGTAAAA 1537
 DB 24 TTCTTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
 LOCUS AZ307896/c
 DEFINITION AZ307896 22 bp DNA linear GSS 29-SEP-2000

DEFINITION IM0010N18F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0010N18 F, genomic survey sequence.
 ACCESSION AZ307896
 VERSION AZ307896.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: N column: 18
 Seq primer: CGTTGTTAAACGACGCCACT
 Clase: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0010N18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCM library"
 /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gll4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 19;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAGCGA 1541
 DB 22 AAAAAAAAAAACAAGCGA 1

RESULT 12
 LOCUS CF308058/c
 DEFINITION ABF--01-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) *Oryza sativa* (japonica cultivar-group) cDNA clone
ABF-01-115, mRNA sequence.
ACCESSION CF308058
VERSION CF308058.1 GI:33679819
KEYWORDS EST.
SOURCE *Oryza sativa* (japonica cultivar-group)
ORGANISM *Oryza sativa* (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehmeriales; Oryzaceae; *Oryza*.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-01-115"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.2%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1510 ACTGTTATTAAAAA 1531
DB 23 AGTGTAGTAAAAA 2

RESULT 13
LOCUS A2627850 24 bp DNA linear GSS 13-DEC-2000
DEFINITION clone UGCG1M0474N20 F, genomic survey sequence.
ACCESSION A2627850
VERSION A2627850.1 GI:11750136
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seq primer: CGGTGTAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0474N20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gblAP129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 AAAAAAAGTAAAGGAA 1542
DB 1 AAAAAAATTAAGAA 22

RESULT 14
LOCUS CF300172/c 23 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza*
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-H15, mRNA
sequence.
ACCESSION CF300172
VERSION CF300172.1 GI:33671933
KEYWORDS EST.
SOURCE *Oryza sativa* (japonica cultivar-group)
ORGANISM *Oryza sativa* (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehmeriales; Oryzaceae; *Oryza*.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355


```

RESULT 18
LOCUS      AL038845
DEFINITION DKF2P566P1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION  AL038845
VERSION    AL038845.1 GI:49682220
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES   source
            1..20
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKF2P566P1746"
            /tissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_lib="566 (synonym: hfkcd2)"
            /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1518 TTTAAAAAAAGTAAAGG 1537
        |||||
        1 TTTAAAAAAAGTAAAGG 20

RESULT 19
LOCUS      CF298207
DEFINITION 7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
sequence.
ACCESSION  CF298207
VERSION    CF298207.1 GI:33669968
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatroidae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES   source
            1..20
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-H23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1521 AAAAAAAAGTAAAGG 1540
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        1 AAAAAAAAGTAAAGG 20

RESULT 20
LOCUS      AZ849506
DEFINITION 2M0150P21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG2M0150P21 R, genomic survey sequence.
ACCESSION  AZ849506
VERSION    AZ849506
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn, D., Aoyagi, A., Barber, M., Beacon, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES   source
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUCG2M0150P21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAGTAAAA 1537
|||||
Db 1 TTTAAAAAAGTAAAA 20

RESULT 21
AZ943299 21 bp DNA linear GSS 26-APR-2001
LOCUS 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0203K21 R, genomic survey sequence.
ACCESSION AZ943299
VERSION AZ943299.1 GI:13807290
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduan@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: K column: 21
Seq primer: CACACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203K21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1521 AAAAAAAAAAGTAAAAAGG 1540
|||||
Db 21 AAAAAAAAAAAAAAAAAAGG 2

RESULT 22
AL038477 22 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZ0566C1646 r1.566 (synonym: hfk42) Homo sapiens cDNA clone
DEFINITION DKFZ0566C1646, mRNA sequence.
ACCESSION AL038477
VERSION AL038477.1 GI:49682139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
Ockenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ockenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ0566C1646"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2bblue"
/clone_lib="566 (synonym: hfk42)"
/note="Vector: pMPL; Site_1: Noci; Site_2: Sali"

FEATURES
source

Query Match 1.2%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAGTAAAA 1537
|||||
Db 1 TTTAAAAAAGTAAAA 20

RESULT 23
CF310486 22 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-c16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-c16, mRNA sequence.
ACCESSION CF310486
VERSION CF310486.1 GI:33682247
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers
 1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--05-C16"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABP)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 2 TTTAAAAAAAGTAAAA 21

RESULT 24 CF339694 23 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--05-B19.B1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
 sequence.

ACCESSION CF339694 GI:33807601
 VERSION CF339694
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--05-B19"
 /issue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 23 TTTAAAAAAAGTAAAA 4

RESULT 25 CF333801 23 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--02-N11.G1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--02-N11, mRNA sequence.

ACCESSION CF333801 GI:33815910
 VERSION CF333801
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--02-N11"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 23 TTTAAAAAAAGTAAAA 4

RESULT 26 AJ668301 24 bp mRNA linear EST 28-JUN-2004
 LOCUS AJ668301 CSEGRAN09 Sub scrofa cDNA clone C000045_P10, mRNA
 DEFINITION sequence.

ACCESSION AJ668301 GI:49352752
 VERSION EST
 KEYWORDS
 SOURCE
 ORGANISM
 Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
 AUTHORS Anderson, S.I., Fanlayson, H.A. and Archibald, A.L.
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options. Vector: pBlueScriptII(KS+). R. Site 1: EcORI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK. EH25 9PS, www.arkgenomics.org.

FEATURES
 source
 1..24
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0000045_P10"
 /issue_type="Placenta"
 /clone_id="CSEQRN09"
 /note="Vector: pBlueScriptII(KS+); Site 1: EcORI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 1.2%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

cy 1518 TTTAAAAAAAAGTAAA 1537
 db 21 TTTAAAAAAAAGTAAA 2

RESULT 27
 BX550903/c 23 bp mRNA linear EST 10-OCT-2003
 LOCUS BX550903 Glossina morsitans moritans adult infected gut Glossina
 DEFINITION morsitans moritans cDNA clone Tse115e01_gtc, mRNA sequence.
 ACCESSION BX550903
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Glossina morsitans moritans
 Glossina morsitans moritans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans moritans and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,

University of Wales,
 Bangor LL57 2UW
 All clones with suffix gtc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES
 source
 1..23
 /organism="Glossina morsitans moritans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse115e01_gtc"
 /issue_type="adult infected gut"
 /clone_id="Glossina morsitans moritans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.2%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

cy 1514 TTTATTTAAAAAAAAGTAAA 1536
 db 23 TTTTAAAAAAAAGTAAA 1

RESULT 28
 BX568055/c 23 bp mRNA linear EST 14-OCT-2003
 LOCUS BX568055 Glossina morsitans moritans adult infected gut Glossina
 DEFINITION morsitans moritans cDNA clone Tse91f03_gtc, mRNA sequence.
 ACCESSION BX568055
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Glossina morsitans moritans
 Glossina morsitans moritans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans moritans and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix gtc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES
 source
 1..23
 /organism="Glossina morsitans moritans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse91f03_gtc"
 /issue_type="adult infected gut"
 /clone_id="Glossina morsitans moritans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Best Local Similarity 82.6%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAAGGAA 1542
Db 23 AAAAAAAAAAGAAAAAAAAA 1

RESULT 31
A2654747/c 19 bp DNA linear GSS 14-DEC-2000
LOCUS A2654747
DEFINITION 1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION A2654747
VERSION A2654747.1 GI:11791893
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529F08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAATATAA 2

RESULT 32
A2343730 20 bp DNA linear GSS 29-SEP-2000
LOCUS A2343730/c
DEFINITION 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION A2343730
VERSION A2343730.1 GI:10422288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: E column: 20
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
 DB 18 AAAAAAAAAAGAAAA 1

RESULT 33
 LOCUS BX548564/c
 DEFINITION BX548564 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse101903_plc, mRNA sequence.
 ACCESSION BX548564
 VERSION BX548564.1 GI:33298798
 KEYWORDS EST.
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 21)
 Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
 source Location/Qualifiers
 1..21
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse101903_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.2%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 94.4%; Pred. No. 31;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
 DB 18 AAAAAAAAAAGAAAA 1

RESULT 34
 LOCUS TA303G05P
 DEFINITION T. brucei sheared genomic DNA clone 303G05, forward sequence, genomic survey sequence.
 ACCESSION AL497383
 VERSION AL497383.1 GI:11865504
 KEYWORDS GSS.
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 TITLE Direct Submision
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: neisayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source Location/Qualifiers
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="Genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="303G05"

Query Match 1.2%; Score 16.4; DB 1; Length 22;
 Best Local Similarity 94.4%; Pred. No. 33;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
 DB 1 AAAAAAAAAAGAAAA 18

RESULT 35
 LOCUS BX564412/c
 DEFINITION BX564412 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse71e10_plc, mRNA sequence.
 ACCESSION BX564412
 VERSION BX564412.1 GI:33431592
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 21)
 Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
source
Location/Qualifiers
1. .21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse71e10_pic"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1517 ATTAAAAAAAAAGTAAA 1537
|||||
21 ATTCAAAAAAAAAAAAAA 1

RESULT 36
AZ308846/c 21 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0012H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0012H15 F, genomic survey sequence.
ACCESSION
AZ308846
VERSION
AZ308846.1 GI:10349246
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTGTAAACGACGCGCAGT
Classes: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAGCG 1540
|||||
21 AAAAAAAAAACAAAAGG 1

RESULT 37
AZ493766
LOCUS
DEFINITION
1M0328C1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328C1 R, genomic survey sequence.
ACCESSION
AZ493766
VERSION
AZ493766.1 GI:10667750
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: C column: 11
Seq primer: CACACAGAAACAGCTATGACC
Classes: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0328C1"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 1517 ATTAAAAAAAAAAGTAAA 1517
Db 1 ATAAAAAAAAAAAAAAAAAAAA 21

RESULT 38
LOCUS AZ513902 21 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0360A13 F, genomic survey sequence.
ACCESSION AZ513902
VERSION AZ513902.1 GI:10695218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 545 TGTGTCGTCGTCGTCGTCGTC 565
Db 21 TGTGTCGTCGTCGTCGTCGTC 1

RESULT 39
LOCUS AZ626965 21 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0467E15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0467E15 R, genomic survey sequence.
ACCESSION AZ626965
VERSION AZ626965.1 GI:11749155
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: B column: 15
Seq primer: CACACAGAAACACCTATGAC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 542 TGTGTGGGTCGTCGTGCGTG 562
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 40
AA911173/c 22 bp mRNA linear EST 09-JUN-1998
LOCUS OK61a10.61 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1520346.3
DEFINITION similar to TR:Q34192 Q34192 NADH DEHYDROGENASE SUBUNIT 5. ;, mRNA sequence.

ACCESSION AA911173 GI:3050463
VERSION AA911173
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 22)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-rc@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI, at:
www-bio.illn.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 520 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amerham
High quality sequence stop: 1.

FEATURES
SOURCE location/Qualifiers

1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1520346"
/lab_host="MDH10B"
/clone_lib="NCI CGAP Kid3"
/note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 1.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1240 TCCTCATCTTGTGTTGTTT 1260
Db 22 TCCTTCCTTGTGTTGTTGT 2

RESULT 41
A2662734 23 bp DNA linear GSS 14-DEC-2000
LOCUS IM0542D04F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0542D04 F, genomic survey sequence.

ACCESSION A2662734
VERSION A2662734
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: D column: 04
Seq primer: CGTTGTTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE location/Qualifiers

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0542D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1511 CTGTTAATTAAAAA 1531

Db 2 CTACTAATAATATAAAAAAAAAA 22

RESULT 42
AZ801003 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M059J16F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M059J16 F, genomic survey sequence.
ACCESSION AZ801003
VERSION AZ801003.1 GI:12953326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: J column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1517 ATTAAAAAAGTAAAA 1537
|||||

Db 1 ATAAAAA 21

RESULT 43
AZ956341/c 21 bp DNA linear GSS 27-APR-2001
LOCUS 2M022H16R Mouse 10kb plasmid UGCG2M library Mus musculus genomic
DEFINITION clone UGCG2M022H16 R, genomic survey sequence.
ACCESSION AZ956341
VERSION AZ956341.1 GI:13827568
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: H column: 16
Seq primer: CACACAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M022H16"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1069 TATTTTCAGTATACA 1084
|||||
19 TATTTTCAGTATACA 4

RESULT 44
AZ345795
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ345795 19 bp DNA linear GSS 29-SEP-2000
M0080H09R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0080H09 R, genomic survey sequence.
AZ345795
AZ345795.1 GI:10425032
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0080H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]AF129072.1), a copy-number
inductible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAA 1536
|||||
Db 1 TTAATAAAAAAAAAAAAAA 19

RESULT 45
AZ650575
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ650575 19 bp DNA linear GSS 14-DEC-2000
M0520P13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0520P13 R, genomic survey sequence.
AZ650575
AZ650575.1 GI:11785200
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0520P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb]AF129072.1), a copy-number
inductible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAA 1536
|||||
Db 1 TTAATAAAAAAAAAAAAAA 19

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RESULT 46
LOCUS      AL038427
DEFINITION DKFZP566A1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION  AL038427
VERSION     DKFZP566A1746, mRNA sequence.
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
             Wiemann, S.
TITLE        OTTENWAEELDER, et al.)
JOURNAL     Unpublished (1999)
COMMENT      MIPS
FEATURES
SOURCE
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566A1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1519 TAAAAAAGTAAAA 1537
Db      1 TAAAAAAGTAAAA 19

RESULT 47
LOCUS      AL038429
DEFINITION DKFZP566A1946.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION  AL038429
VERSION     DKFZP566A1946, mRNA sequence.
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
             Wiemann, S.
TITLE        OTTENWAEELDER, et al.)
JOURNAL     Unpublished (1999)
COMMENT      MIPS
FEATURES
SOURCE
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566A1946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566A1946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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Query Match      1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1519 TAAAAAAGTAAAA 1537
Db      1 TAAAAAAGTAAAA 19

RESULT 48
LOCUS      AL038570
DEFINITION DKFZP566F1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION  AL038570
VERSION     DKFZP566F1746, mRNA sequence.
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
             Wiemann, S.
TITLE        OTTENWAEELDER, et al.)
JOURNAL     Unpublished (1999)
COMMENT      MIPS
FEATURES
SOURCE
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566F1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566F1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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RESULT 49
LOCUS      AL587759/c
DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  AL587759
VERSION     ROS061G06, mRNA sequence.
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
             Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Murray, F.
TITLE        BP Chicken Brain Library
JOURNAL     Unpublished (2001)
COMMENT      Dept. Genomics and Bioinformatics
             Roslin Institute
             Roslin, Midlothian, EH25 9PS, UK
             Tel: +44 (0)131 527 4200
             Fax: +44 (0)131 440 0434
```

Email: frazer.murray@bsrc.ac.uk
GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech

Seq primer: M13F.

FEATURES

SOURCE

Location/Qualifiers

1..20

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS061G06"

/tissue_type="Brain"

/dev_stage="Unknown"

/lab_host="DH10B"

/clone_lib="BP Chicken Brain Library"

/note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; Cloned

unidirectionally. Primer: Oligo dt. 5' adaptor sequence:

5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'

GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from

Clontech (*6854-1)"

Query Match 1.1%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 43;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAG 1537

Db 20 TAAAAAAGTAAAG 2

RESULT 50

AZ45856/c

LOCUS 20 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0080G1R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone UGCG1M0080G17 R, genomic survey sequence.

ACCESSION

AZ45856

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

LOCATION/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0080G17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1473214|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 43;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 TAAAAAAGTAAAG 1538

Db 20 TAAAAAAGTAAAG 2

RESULT 51

AZ486784/c

LOCUS 20 bp DNA linear GSS 05-OCT-2000

DEFINITION 1M0315C20F Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone UGCG1M0315C20 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

LOCATION/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0315C20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1473214|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAATAAAAGTAA 1537
|||||
Db 20 TAAATAAAAGTAA 2

RESULT 52
LOCUS A2858419 20 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M163003R Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION A2858419
VERSION A2858419.1 GI:13051545
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 Row: 0 Column: 03
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
Location/Qualifiers

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAATAAAAGTAA 1537
|||||
Db 1 TAAATAAAAGTAA 19

RESULT 53
LOCUS AL048772 21 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP566N143.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION AL048772
VERSION AL048772.1 GI:4727843
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

FEATURES
Location/Qualifiers

1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL1-Blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not; Site_2: SalI"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 GTTAATTAATAAA 1531
|||||
Db 2 GTTAATAAA 20

RESULT 54
LOCUS CF318152/c 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-C11, mRNA sequence.
ACCESSION CF318152

```

VERSION      CF318152.1  GI:33689913
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc., Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-08-C11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.Coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: ECORI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAAGTAAAG 1538
Db      19 AAAAAAAAAAAGTAAAG 1

RESULT 55
CN546489/c      21 bp      mRNA      linear      EST 30-APR-2004
LOCUS           EST 18633 Ripe Grape Berry Lambda Triplex2 library Vitis vinifera
DEFINITION     CDNA clone B3CS57RB007E11 3', mRNA sequence.
ACCESSION      CN546489
VERSION        CN546489.1  GI:46911114
KEYWORDS       EST.
SOURCE         Vitis vinifera
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Abadl,P., Agase,A., Ageorges,A., Atanassova,R., Barrieu,F.,
              Couture,C., Dedaldechamp,F., Delrot,S., Gillsant,D., Grimplet,J.,
              Hamdi,S., Romieu,C. and Terrier,N.
TITLE          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
              UMR 619 - Equipe Biologie de la Vigne
              Universite de Bordeaux I, Institut National de la Recherche
              Agronomique
              71, Avenue Edouard Bourleaux, BP 81, 33683 Villenave D'Ornon Cedex,
              France
              Tel: 00-33-(0)5-57-12-25-50

```

```

FEATURES
source
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007E11"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1519 TAAAAAAAAAAGTAAA 1537
Db      21 TAAAAAAAAAAGTAAA 3

RESULT 56
AZ610868/c      21 bp      DNA      linear      GSS 13-DEC-2000
LOCUS           IN0436G12F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
DEFINITION     clone UNGC1M0436G12 F, genomic survey sequence.
ACCESSION      AZ610868
VERSION        AZ610868.1  GI:11733058
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weis,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weis
              University of Utah Genome Center
              University of Utah
              Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert length: 10000 Std error: 0.00
              Plate: 0436 row: G column: 12
              Seq primer: CGTTGTAAACGACGCGCACT
              Class: plasmid ends
              High quality sequence stop: 21.

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG1M0436G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

```


was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAA 1536
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 57
A2764492 21 bp DNA linear GSS 16-FEB-2001
LOCUS JMO56DD04R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M056DD04 R, genomic survey sequence.
ACCESSION A2764492
VERSION A2764492.1 GI:12879511
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 04
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
Source 1. .21
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M056DD04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAA 1536
Db 3 TTAATAAAAAAAAAAAAAA 21

RESULT 58
BX556059 22 bp mRNA linear EST 10-OCT-2003
LOCUS BX556059/c
DEFINITION BX556059 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse24f09_p1c, mRNA sequence.
ACCESSION BX556059
VERSION BX556059.1 GI:33380008
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 22)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
MEDLINE
PUBMED

JOURNAL
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
Location/Qualifiers

FEATURES
Source 1. .22
Location/Qualifiers

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:17546"
/clone="Tse24f09_p1c"
/tissue_type="adult infected gut"
/clone_1lb="Glossina morsitans morsitans adult infected
gut"
/note="Country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAAAGTAAAA 1537
 |||||
 Db 20 TAAAAAAAAAAAAAAAAAAAA 2
 |||||

RESULT 59
 CF310806/c 22 bp mRNA linear EST 15-AUG-2003
 LOCUS
 DEFINITION ABF-05-K20-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone ABF-05-K20, mRNA sequence.
 ACCESSION CF310806
 VERSION CF310806.1 GI:33682567
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-05-K20"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 48;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1522 AAAAAAAAAAAGTAAAGCG 1540
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAGCG 4
 |||||

RESULT 60
 COT78290 22 bp mRNA linear EST 05-AUG-2004
 LOCUS
 DEFINITION BLOC3B H01 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum cDNA 5' similar to hypothetical protein, mRNA sequence.
 ACCESSION COT78290
 VERSION COT78290.1 GI:50994270
 KEYWORDS EST.
 SOURCE Ambystoma mexicanum (axolotl)
 ORGANISM Ambystoma mexicanum
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae; Ambystoma.
 REFERENCE 1 (bases 1 to 22)
 Habermann,B., Bebin,A.G., Herklotz,S., Volkmmer,M., Eckelt,K.,

TITLE
 JOURNAL
 COMMENT
 Tanaka Lab
 Max Planck Institute of Molecular Cell Biology and Genetics, Dresden
 Proteinhauterstrasse 108, 01307 Dresden, Germany
 Tel: 0049 351 210 2620
 Fax: 0049 351 210 1489
 Email: tanaka@mpi-cbg.de
 Plate: BLOC3B row: 01 column: H
 Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
 Location/Qualifiers
 1..22
 /organism="Ambystoma mexicanum"
 /mol_type="mRNA"
 /db_xref="taxon:8296"
 /tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
 /note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI; Unormalized cDNA plasmid library prepared by Invitrogen. Site fractionated mRNA was polydT primed and cloned into NotI-SalI site of pCMVSPORT6. Bacterial host is EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DAXBL"

Query Match 1.1%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 48;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAG 1538
 |||||
 Db 4 AAAAAAAAAAAAAAAAAAG 22
 |||||

RESULT 61
 A2823875 22 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0098K07F Mouse 10kb plasmid UGCIM library Mus musculus genomic clone UDC2M0098K07 F, genomic survey sequence.
 ACCESSION A2823875
 VERSION A2823875.1 GI:12993795
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0098 row: K column: 07
 Seq primer: CGATTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0098K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
Db 4 AAAAAAAAAAAG 22

RESULT 62
LOCUS BH000233 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0287121R Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0287121 R, genomic survey sequence.
ACCESSION BH000233
VERSION BH000233.1 GI:13871459
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0287 row: 1 column: 21
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers 1. .22

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0287L21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
Db 3 AAAAAAAAAAAG 21

RESULT 63
LOCUS A1708831 22 bp mRNA linear EST 04-JUN-1999
DEFINITION aa27d12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318423 3' similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION A1708831
VERSION A1708831.1 GI:4998607
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Scheinberg,K., Stepcoe,M., Tan,F., Thaising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE Washu-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40up from Gibco
High quality sequence stop: 1.
Location/Qualifiers 1. .22

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"

/clone_1lb="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carlini organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 9/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dt priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
 DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 67
 CF299342/c
 LOCUS 7LEAF--03-F06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION active (japonica cultivar-group) cDNA clone 7LEAF--03-F06, mRNA
 sequence.

ACCESSION
 VERSION CF299342
 CF299342.1 GI:33671103
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE CONTACT: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--03-F06"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
 DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 68
 CF300133/c
 LOCUS 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION active (japonica cultivar-group) cDNA clone 7LEAF--04-G19, mRNA
 sequence.

ACCESSION
 VERSION CF300133
 CF300133.1 GI:33671894
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE CONTACT: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--04-G19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
 DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 69
 CF310366/c
 LOCUS ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--04-P14, mRNA sequence.

ACCESSION
 VERSION CF310366
 CF310366.1 GI:33682127
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE CONTACT: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers
 1..22
 /organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="ABF-04-P14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="vector: PCR4-TOPO, Site_1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1516 AATTAAAAAAGTAAA 1537
       ||| ||||| |||||
Db      22 AAAAAAAAAAAAAAAAAAA 1

RESULT 70
CP311269/c
LOCUS      CP311269          22 bp    mRNA           linear   EST 15-AUG-2003
DEFINITION ABF--06-G21.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa [japonica cultivar-group] CDNA clone
            ABF--06-G21, mRNA sequence.
ACCESSION  CP311269
VERSION     CP311269.1 GI:33683030
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 22)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyoeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
FEATURES             source
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39847"
                     /clone="ABF-06-G21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="vector: PCR4-TOPO, Site_1: EcoRI, leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

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Oy 1516 AATTAAAAAAGTAAA 1537

Best Local Similarity 81.1%; Score 15.6; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAA 1537

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Db      22 AAAAAAAAAAAAAAAAAAAAAA 1
|-----|
RESULT 71
CF311713                22 bp    mRNA        linear   EST 15-AUG-2003
LOCUS      CF311713
DEFINITION ABF--07-B13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  CF311713
VERSION     CF311713.1 GI:33683474
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, Greengene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myungji University
           Yongin, Kyeonggi, Korea
           Tel.: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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                 /organism="Oryza sativa (japonica cultivar-group)"
                 /mol_type="mRNA"
                 /cultivar="Nackdong"
                 /db_xref="taxon:39947"
                 /clone="ABF--07-B13"
                 /tissue="leaf"
                 /dev_stage="14 days after germination"
                 /lab_host="E.coli DH10B"
                 /clone_id="ABF3-overexpressing transgenic rice plasmid
                 cDNA library (ABF)"
                 /note="Vector: PCR4-TOP0; Site 1: EcoRI; Leaf was dried
                 for 2hrs. Oligo-capped mRNA was reverse transcribed and
                 then used for PCR. mRNA was prepared from ABA-responsive
                 element binding transcription factor 3 overexpression
                 line."

Query Match          1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy      1516 AATTAAATAAGTAAA 1537
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Db      1 AAAAAAAAAAAAAAAAAAAAAA 22
|-----|

RESULT 72
CF312498                22 bp    mRNA        linear   EST 15-AUG-2003
LOCUS      CF312498
DEFINITION ABF--08-B15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  CF312498
VERSION     CF312498.1 GI:33684259
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```


VERSION CF334781.1 GI:33817904
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidaeae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-D05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 76
LOCUS CF336250 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-D20.b1 AcJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
JMT--06-D20, mRNA sequence.
ACCESSION CF336250
VERSION CF336250.1 GI:33820891
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidaeae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..22

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--06-D20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 77
LOCUS CF337580 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-B11.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
JMT--08-B11, mRNA sequence.
ACCESSION CF337580
VERSION CF337580.1 GI:33823547
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidaeae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
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/clone="JMT--08-B11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 78
LOCUS CF338524/c 22 bp mRNA linear EST 18-AUG-2003
DEFINITION RC11--01-P07.g1 Regenerated callus lambda phage cDNA library (RC11)
Oryza sativa (japonica cultivar-group) cDNA clone RC11--01-P07,
mRNA sequence.
ACCESSION CF338524
VERSION CF338524.1 GI:33825436
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RC11--01-P07"
/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RC11)"
/note="Vector: pBluescript SK(+); Site 1: SclI; Site 2:
XhoI; cDNA was inserted into lambda uni-ZAP XR vector at 5'
end with SclI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
LOCUS CN545550/c 22 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003D05 3', mRNA sequence.
ACCESSION CN545550
VERSION CN545550.1 GI:46910175
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosida; Vitaceae; Vitis.
1 (bases 1 to 22)
Abbal,P., Agasee,A., Ageorges,A., Atanassova,R., Barileu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,D.,
Hamdi,S., Komleu,C. and Terrier,N.

TITLE
JOURNAL
COMMENT
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..22
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
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SfiI; Site_2: SliIb; Oriented library"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
LOCUS A2310066/c 22 bp DNA linear GSS 29-SEP-2000
DEFINITION IM001D18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M001D18 R, genomic survey sequence.
ACCESSION A2310066
VERSION A2310066.1 GI:10351682
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0018D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 81
LOCUS A2316361 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0034116F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034116 F, genomic survey sequence.
ACCESSION A2316361
VERSION A2316361.1 GI:10364110
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: 1 column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034116"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 82
LOCUS A2317017/c 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035P09 F, genomic survey sequence.
ACCESSION A2317017
VERSION A2317017.1 GI:10365400
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: 1 column: 09
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22

FEATURES
source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035P09"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%, Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1523 AAAAAAAAAAGTAAAGCGAAG 1544
Db 22 AAAAAAAAAAAAAAAAAAGCGGCG 1

RESULT 83
LOCUS A2351527 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089507 R, genomic survey sequence.
ACCESSION A2351527
VERSION A2351527.1 GI:10430764
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: E column: 07
Seq primer: CACACAGGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089507"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%, Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 84
LOCUS A2357630 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0099M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099M15 F, genomic survey sequence.
ACCESSION A2357630
VERSION A2357630.1 GI:10471318
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: M column: 15
Seq primer: GGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099M15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 85
LOCUS A2388103 22 bp DNA linear GSS 02-OCT-2000
DEFINITION M0147N14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0147N14 R, genomic survey sequence.
ACCESSION A2388103
VERSION A2388103.1 GI:10501811
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: N column: 14
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0147N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 86
LOCUS A2401908/c 22 bp DNA linear GSS 03-OCT-2000
DEFINITION M0168P24R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0168P24 R, genomic survey sequence.
ACCESSION A2401908
VERSION A2401908.1 GI:10516982
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 24
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0168P24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 87
A2424307 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0203A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0203A24 R, genomic survey sequence.
ACCESSION A2424307
VERSION A2424307.1 GI:10548320
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 88
A2428818 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0212A05 R, genomic survey sequence.
ACCESSION A2428818
VERSION A2428818.1 GI:10552831
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0212A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 89
A2459654/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0266G12R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0266G12 R, genomic survey sequence.
ACCESSION A2459654
VERSION A2459654.1 GI:10617779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: G column: 12
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0266G12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 90
A2463503/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0272E24F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0272E24 F, genomic survey sequence.
ACCESSION A2463503
VERSION A2463503.1 GI:10621628
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 24
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0272E24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 93
AZ607658 22 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0430A13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0430A13 F, genomic survey sequence.
ACCESSION AZ607658
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0430 row: A column: 13
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
SOURCE 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0430A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD2nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 94
AZ654691 22 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0529D05F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0529D05 F, genomic survey sequence.
ACCESSION AZ654691
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 05
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
SOURCE 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0529D05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD2nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 95
LOCUS A2760533 22 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 F, genomic survey sequence.
ACCESSION A2760533
VERSION A2760533.1 GI:12868477
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 96
LOCUS A2779844/c 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0016112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0016112 R, genomic survey sequence.
ACCESSION A2779844
VERSION A2779844.1 GI:12910910
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: I column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

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/strain="C57BL/6J"
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/clone="UUGC2M0016112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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electrophoresis. Vector DNA was prepared from a derivative

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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 97
AZ785019/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0028E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0028E04 R, genomic survey sequence.
ACCESSION AZ785019
VERSION AZ785019.1 GI:12921341
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Jellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0028 row: E column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers

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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028E04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 98
AZ787098/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0033A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0033A05 F, genomic survey sequence.
ACCESSION AZ787098
VERSION AZ787098.1 GI:12925520
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Jellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0033 row: A column: 05
Seq primer: GGTTCGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0033A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 99
A2787606/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0034G12P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0034G12 F, genomic survey sequence.
ACCESSION A2787606
VERSION A2787606.1 GI:12926565
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: G column: 12
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UGCG2M0034G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 100
A2792704/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0045A24P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0045A24 F, genomic survey sequence.
ACCESSION A2792704
VERSION A2792704.1 GI:12936911
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 24
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
/organism="Mus musculus"
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/clone="UGCG2M0045A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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polynucleotide kinase. Adaptor oligonucleotides were
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adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAGTAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 101
AZ810674/c 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0092K13R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0076E19 F, genomic survey sequence.

ACCESSION
AZ810674
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: E column: 19
Seq primer: CGTGTGAAACGACGCCGACG
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0076E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAGTAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 102
AZ820439/c 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0092K13R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0092K13 R, genomic survey sequence.

ACCESSION
AZ820439
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: K column: 13
Seq primer: CACACAGAAACGACTGTGAC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0092K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
|||
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 103

AZ841661 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M013918R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M013918 R, genomic survey sequence.

ACCESSION AZ841661
VERSION AZ841661.1 GI:13011569
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: 1 column: 18
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

Source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M013918"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
|||
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 104

AZ843514 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0142124F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0142124 F, genomic survey sequence.

ACCESSION AZ843514
VERSION AZ843514.1 GI:13013422
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: 1 column: 24
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

Source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0142124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1516 AATTAAAAAAGTAAAA 1537
 |||
 22 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 105

AZ946102 22 bp DNA linear GSS 27-APR-2001
 LOCUS TA131B09P
 DEFINITION T. brucei sheared genomic DNA clone 131b09, forward sequence,
 clone UUCG2M0207D13 R, genomic survey sequence.

ACCESSION AZ946102
 VERSION AZ946102.1 GI:13812911
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts

JOURNAL Published (2000)

COMMENT Contact: Robert B. Weis
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0207 row: D column: 13
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

1. .22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0207D13"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCG2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1516 AATTAAAAAAGTAAAA 1537
 |||
 22 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 106

TA131B09P 22 bp DNA linear GSS 13-DEC-2000
 LOCUS TA131B09P
 DEFINITION T. brucei sheared genomic DNA clone 131b09, forward sequence,
 genomic survey sequence.

ACCESSION AL464164
 VERSION AL464164.1 GI:11834427
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

Location/Qualifiers
 1. .22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="131b09"

Query Match 1.1%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 54;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1516 AATTAAAAAAGTAAAA 1537
 |||
 22 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 107

TA329F10P 22 bp DNA linear GSS 13-DEC-2000
 LOCUS TA329F10P
 DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,
 genomic survey sequence.

ACCESSION AL492691
 VERSION AL492691.1 GI:11868830
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

TITLE	JOURNAL	COMMENT
Meville, S.E., Rajandream, M.A. and Barrrell, B.G.		
Direct Submission		
Submitted (10-DEC-2000)	Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA, E-mail: barrrell@sanger.ac.uk and nh@sanger.ac.uk	
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrrell, Oxford University Press, 1999).		
Email: nelsayed@tigr.org		
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .		
Location/Qualifiers		
1..22		
/organism="Trypanosoma brucei"		
/mol_type="genomic DNA"		
/strain="TREU927"		
/db_xref="taxon:5691"		
/clone="329f10"		
Query Match	1.1%	Score 15.6; DB 1; Length 22;
Best Local Similarity	81.8%;	Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Oy	1516	AATTGAAAAAGTAAAA 1537
Db	1	AAAAAAAAAAAAAAAAAAAA 22
RESULT 108		
TA35C120/c		
LOCUS	TA35C120	22 bp DNA linear GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 35c12, reverse sequence,	
ACCESSION	AL454256	
VERSION	AL454256.1	GI:11855060
KEYWORDS	GSS.	
SOURCE	Trypanosoma brucei	
ORGANISM	Trypanosoma brucei	
REFERENCE	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;	
AUTHORS	Trypanosoma.	
1 (bases 1 to 22)		
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Meville, S.E., Rajandream, M.A. and Barrrell, B.G.		
Direct Submission		
Submitted (10-DEC-2000)	Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA, E-mail: barrrell@sanger.ac.uk and nh@sanger.ac.uk	
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrrell, Oxford University Press, 1999).		
Email: nelsayed@tigr.org		
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .		
Location/Qualifiers		
1..22		
/organism="Trypanosoma brucei"		
/mol_type="genomic DNA"		
/strain="TREU927"		

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/db xref="taxon:5691"
/clone="j35c12"

Query Match          1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy      1516 AATTAAAAAAAGTAAAA 1537
      ||| ||||| ||||| |||||
Db      22 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 109
LOCUS      TA380A07P          22 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 380a07, forward sequence,
ACCESSION  AL497713
VERSION     AL497713.1 GI:11873435
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Trypanosoma brucei
            Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GMTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
            Location/Qualifiers
                1..22
                   /organism="Trypanosoma brucei"
                   /mol_type="genomic DNA"
                   /strain="TREU927"
                   /db_xref="taxon:5691"
                   /clone="380a07"

FEATURES
source
    1..22
       /organism="Trypanosoma brucei"
       /mol_type="genomic DNA"
       /strain="TREU927"
       /db_xref="taxon:5691"
       /clone="380a07"

Query Match          1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy      1516 AATTAAAAAAAGTAAAA 1537
      ||| ||||| ||||| |||||
Db      1 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 110
LOCUS      AG194579          22 bp      DNA      linear      GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-072N05.T0, genomic survey
ACCESSION  AG194579
VERSION     AG194579.1 GI:45226755
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

TITLE Park H., Kim Y., Kim S., Han Y., Woo T., Park K., Eun C.J.,
JOURNAL Moon S.T., Chu M., Kim H., Joo S., Kim C., Song W. and Yoo H.
REFERENCE BAC end sequences of Library Rp-43

AUTHORS Unpublished

TITLE 2 (bases 1 to 22)

JOURNAL Park H., Kim Y., Kim S., Han Y., Woo T., Park K., Eun C.J.,
AUTHORS Moon S.T., Chu M., Kim H., Joo S., Kim C., Song W. and Yoo H.
TITLE Direct Submission

COMMENT Submitted (07-JUN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-335, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: TV

LIBRARY

Vector : pBACE3.6

R.Site 1 : ECORI

R.Site 2 : EcoRI

Location/Qualifiers

1..22

/organism="Pan troglodytes"

/mol_type="Genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-072N05-TV"

/sex="male"

/cell_type="lymphocytes"

/clone_id="RP-43 Chimpanzee Male BAC Library"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 54;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1516 AATTAAAAAAGTAA 1537

Dd 1 AAAAAAAAAAAAAAAAAA 22

RESULT 111 CF334610/c 19 bp mRNA linear EST 18-AUG-2003

CF334610/c LOCUS DEFINITION JMT-03-P13.b1 ACJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone JMT-03-P13, mRNA sequence.

ACCESSION CF334610

VERSION CF334610.1 GI:33817556

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,Y.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myoung University
Yongin, Kyoeongi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES SOURCE Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

Query Match	1.1%;	Score 15.4;	DB 1;	Length 19;
Best Local Similarity	94.1%;	Pred. No. 53;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1515	TAATTAATAAAAAAAAAA	1531	
Db	19	TAATTAATAAAAAAAAAA	3	
RESULT 112				
CL680297/c				
LOCUS	CL680297	20 bp	DNA	linear
DEFINITION	PR10128C.G05.2 - PR10128C.BR (20) Note: Recurring String Mixed			
ACCESSION	pacificus fosmid_library of P. pacificus var. California Pristionchus			
VERSION	CL680297			
KEYWORDS	CL680297.1 GI:50187127			
SOURCE	GSS.			
ORGANISM	Pristionchus pacificus			
	Pristionchus pacificus			
	Eukaryote; Metazoa; Nematoda; Chromadorea; Diplogasterida;			
	Neodiplogasteridae; Pristionchus.			
	1 (bases 1 to 20)			
AUTHORS	Stinivaasen J., Otto G.W., Kahlow U., Geisler R. and Sommer R.J.			
TITLE	AppaB: an AcceB database for the nematode satellite organism			
JOURNAL	Pristionchus pacificus			
COMMENT	Nucleic Acids Res. 32 (1), D421-D422 (2004)			
	Contact: Sommer RJ			
	Evolutionary Biology			
	Max-Planck-Institute for Developmental Biology			
	Spemannstr. 37-39, Tuebingen D-72076, Germany			
	Tel.: 00497071601371			
	Fax: 00497071601498			
	Email: ralf.sommer@tuebingen.mpg.de			
	This library was generated at Caltech, Pasadena, USA and end			
	sequenced at Vancouver, Canada.			
	Seq primer: T7			
	Class: fosmid ends.			
FEATURES				
Source	Location/Qualifiers			
	1..20			
	/organism="Pristionchus pacificus"			
	/mol_type="genomic DNA"			
	/strain="California"			
	/db_xref="taxon:54126"			
	/clone_lib="Mixed stage fosmid library of P. pacificus			
	var. California"			
	/note="Vector: pGP108-5 Fosmid vector"			
Query Match	1.1%;	Score 15.4;	DB 1;	Length 20;
Best Local Similarity	94.1%;	Pred. No. 56;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1521	AAAAAAAAAAGTAAAA	1537	
Db	20	AAAAAAAAAAGAAAAA	4	
RESULT 113				
CF319122/c				
CF319122	21 bp	mRNA	linear	EST 15-AUG-2003

DEFINITION HD--09-107.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--09-107, mRNA sequence.

ACCESSION CF319122.1 GI:33690883

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..21

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-09-107"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.1%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1521 AAAAAAAAAAGTAAA 1537

Db 17 AAAAAAAAAAAATAAA 1

RESULT 114

T49097

LOCUS T49097 25 bp mRNA linear EST 06-FEB-1995

DEFINITION yb08h08.s1 StrataGene placenta (#937225) Homo sapiens cDNA clone IMAGE:70623 3' similar to gb:K62744 CLASS II

HISOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097

VERSION T49097.1 GI:650957

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 25)

1 Hlller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B., Chlasoe,S., Dietrich,N., Dubuque,T., Favell,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Maris,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Ronfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 8889549

COMMENT Other ESTs: yb08h08.r1

Contact: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High galley sequence stops: 1

High galley sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21m13

High quality sequence stop: 1.

location/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:491520"

/db_xref="taxon:9606"

/clone="IMAGE:70623"

/sex="male"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="StrataGene placenta (#937225)"

/note="Organ: placenta; Vector: pluescript SK-, Site 1: EcoRI, Site 2: XhoI, Cloned unidirectionally. Primer: Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GATTGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

Query Match 1.1%; Score 15.4; DB 1; Length 25;
Best Local Similarity 76.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1302 TCTATTTTATTTTCAGACG 1326

Db 1 TTTTCTTTTCTTTTAAAGAA 25

RESULT 115

LOCUS AL038460 20 bp mRNA linear EST 06-JUL-2004

DEFINITION DKFZP56B2246.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZP56B2246, mRNA sequence.

ACCESSION AL038460

VERSION AL038460.1 GI:49682131

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 20)

1 Otenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Otenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neubherg, Germany.

location/Qualifiers

1..20

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZP56B2246"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="X1-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1, Site 1: NotI, Site 2: SalI"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1518 TTTAAAAAAGTAAAA 1537
 Db 1 TCAAAAAAAAAAAAAA 20

RESULT 116
 CF298018/c 20 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA
 sequence.

ACCESSION CF298018
 VERSION CF298018.1 GI:33669779
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Oryza sativa (japonica cultivar-group)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--01-D19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1516 AATTAAAAAAGTAA 1535
 Db 20 AATCAAAAAAAAAAAAAA 1

RESULT 117
 CF339443 20 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--04-003.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-003,
 mRNA sequence.
 ACCESSION CF339443
 VERSION CF339443.1 GI:33827271
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Oryza sativa (japonica cultivar-group)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--04-003"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E. coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 424 GTGGCGGCTCGCGCGCGC 443
 Db 1 GCGGCGGCGAGCGCGCGCGC 20

RESULT 118
 A0661013/c 21 bp mRNA linear EST 28-JUN-2004
 LOCUS A0661013 CSEORAN09 Sus scrofa cDNA clone C0000935_H04, mRNA
 DEFINITION sequence.
 ACCESSION A0661013
 VERSION A0661013.1 GI:49345046
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

REFERENCE 1 (bases 1 to 21)
 Anderson,S.T., Finlayson,H.A. and Archibald,A.L.
 Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 Unpublished (2004)
 JOURNAL Contact: Anderson ST
 COMMENT Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -minscore 20
 and -mismatch 12 options. Vector:pBluescriptII (KS+) R. Site 1:
 EcoRI R. Site 2: NotI Description: Normalised library constructed
 from pooled tissue from day 30 placentas. Clones available from UK
 Centre for Functional Genomics in Farm Animals, Roslin Institute,
 Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
 source 1..21
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"

```
/clone="C0000935.H04"
/tissue_type="placenta"
/clone_id="CSROBAM09"
/Note=Vector: pBluescriptII(KS+), Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match      1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1512 TGTAAATTAATAAAAAAAAA 1531
DB      20 TTTTATTAATAAAAAAAAAA 1

RESULT 119
AL038582      AL038582      21 bp mRNA linear EST 06-JUL-2004
LOCUS      DKFZP566F0946.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION      DKFZP566F0946, mRNA sequence.
ACCESSION      AL038582
VERSION      AL038582.1 GI:49682163
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566F0946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_id="566 (synonym: hfkcd2)"
/Note=Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match      1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1518 TTAATAAAAAAAAAAGTAAAA 1537
DB      1 TCATAAAAAAAAAAAAAAAAAA 20

RESULT 120
AL038627      AL038627      21 bp mRNA linear EST 06-JUL-2004
LOCUS      DKFZP566H2046.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION      DKFZP566H2046, mRNA sequence.
ACCESSION      AL038627
VERSION      AL038627.1 GI:49682173
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
```

```
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566H2046"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_id="566 (synonym: hfkcd2)"
/Note=Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match      1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1518 TTAATAAAAAAAAAAGTAAAA 1537
DB      1 TCATAAAAAAAAAAAAAAAAAA 20

RESULT 121
AL038839      AL038839      21 bp mRNA linear EST 06-JUL-2004
LOCUS      DKFZP566P1346.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION      DKFZP566P1346, mRNA sequence.
ACCESSION      AL038839
VERSION      AL038839.1 GI:49682218
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566P1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_id="566 (synonym: hfkcd2)"
/Note=Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match      1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1518 TTAATAAAAAAAAAAGTAAAA 1537
DB      1 TCATAAAAAAAAAAAAAAAAAA 20

RESULT 122
CF330439/c      CF330439      21 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone NACL--06-C12, mRNA
sequence.
ACCESSION      CF330439
```

VERSION CE330439.1 GI:33809110
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatoidae; Oryzaceae; Oryza.
 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..21
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-C12"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 66;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1512 TGTAAATTAATAAAAAAAAAA 1531
 ||||| ||||| ||||| |||||
 21 TGTATATAAAAAAAAAAAAAA 2

RESULT 123 21 bp mRNA linear EST 20-MAY-2004
 CN763587
 LOCUS ID0AAA7BH12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA7BH12 5',
 DEFINITION mRNA sequence.
 ACCESSION CN763587
 VERSION CN763587.1 GI:47537510
 KEYWORDS EST.
 SOURCE Acyrthosiphon pisum (pea aphid)
 ORGANISM Acyrthosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
 1 (bases 1 to 21)
 Hunter,W., Martinez-Torres,D., Rabhe,Y., Sabater-Munoz,B.,
 Stern,D., Tagu,D. and Wincker,P.
 An expressed sequence tags database for the pea aphid Acyrthosiphon
 pisum
 Unpublished (2004)
 JOURNAL Contact: D. Tagu
 COMMENT INRA Rennes
 UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
 Tel: +33-2-23.48.51.65
 Fax: +33-2-23.48.51.50
 Risk of contamination by bacterial sequences from obligatory
 (Buchnera) or facultative endosymbionts. These sequences were
 obtained in the frame of the International Consortium of Aphid
 Genomics in collaboration with Genoscope
 PCR Primers
 FORWARD: CAGGAAACAGCTATGACC

FEATURES Plate: 7 row: H column: 12.
 SOURCE Location/Qualifiers
 1..21
 /organism="Acyrthosiphon pisum"
 /mol_type="mRNA"
 /cultivar="developmentstage"
 /db_xref="taxon:7029"
 /clone="ID0AAA7BH12"
 /tissue_type="whole insect"
 /dev_stage="nymphs and adults (parthenogenetic females)"
 /lab_host="Xrl-Blue"
 /clone_lib="ApMS"
 /note="Vector: PBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
 Sample name: ID0AAA; Plant growth place: Department of
 Ecology & Evolutionary Biology, Princeton University
 Soil conditions: Soil; Sowing date: 01/06/1999;
 Harvesting date: 01/06/1999; Stress date: no stress;
 Description: Aphids inoculated on one-week old *Vicia faba*
 under non-sterile conditions. All parthenogenetic stages
 and both winged and wingless adults were collected for
 library construction. ; experimental condition: long
 photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 66;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1512 TGTAAATTAATAAAAAAAAAA 1531
 ||||| ||||| ||||| |||||
 2 TTTTATTAATAAAAAAAAAA 21

RESULT 124 21 bp DNA linear GSS 03-OCT-2000
 AZ393269
 LOCUS ID0156F13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0156F13 F, genomic survey sequence.
 ACCESSION AZ393269
 VERSION AZ393269.1 GI:10508341
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weis
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0156 row: F column: 13
 Seq primer: CGTGTGTAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCIM0156F13"
 /sex="Male"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gbl|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1339 AATTACTATTTTATTTT 1358
Db 1 AATTAGTATTTTATTTT 20

RESULT 125

AZ625662 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0465C23F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0465C23 F, genomic survey sequence.

ACCESSION AZ625662
VERSION 1
KEYWORDS GSS: 11747852

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C.,

Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00

Plate: 0465 row: C column: 23
Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0465C23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

FEATURES
source

/clone lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gbl|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1301 ATCTATTTTATTTTCA 1320
Db 20 AATATTTTTTTTTTTT 1

RESULT 126

CF300172 23 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--04-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-H15, mRNA
sequence.

ACCESSION CF300172
VERSION 1
KEYWORDS EST: 33671933

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehbaritoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,

Song, S.-I., Kim, J.-K., Kim, Y.-K., and Nahm, B.-H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL Contact: Nahm B.-H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

/db_xref="taxon:39847"
/clone="7LEAF--04-H15"

/tissue_type="leaf"
/dev_stage="7 days after germination"

/lab_host="E. coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO. Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

FEATURES
source

Query Match 1.1%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 72;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1248 TTTGTTGTTTAAATCA 1267
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 Db 1 TTTTITTTTTTTTATTA 20

RESULT 127
 AM245585/c 15 bp mRNA linear EST 07-JAN-2000
 LOCUS DEFINITION 2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3',
 mRNA sequence.

ACCESSION AM245585
 VERSION AM245585.1 GI:6588578
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2822740.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-rc@mail.nih.gov
 Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LINI) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LINI at:
 www-bio.lnli.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
 PHRED high quality bases following vector sequence. Very low
 Quality Sequence: Trace file contained 15 contiguous distinct peaks
 following vector sequence. Polyadenylation: Based upon the presence
 of a XhoI site followed by a run of 14 or more T residues at the
 beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: LICM10 row: D column: 5
 High quality sequence stop: 6.

FEATURES

source location/Qualifiers

1..15
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2822740"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the Laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.1%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1515 TAAATTAATAAAAAA 1529
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 Db 15 TAAATTAATAAAAAA 1

RESULT 128

A2774536 19 bp DNA linear GSS 16-FEB-2001
 LOCUS DEFINITION 2M0004P01F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 clone UGCLM0004P01 F, genomic survey sequence.

ACCESSION A2774536
 VERSION A2774536.1 GI:12900089
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0004 row: P column: 01
 SEQ PRIMER: CGTTGTAAACGACGCGCACT
 CLASS: plasmid ends
 High quality sequence stop: 19.

FEATURES

source location/Qualifiers

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0004P01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473214|g5|AFL29072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 15; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAAAAG 1532
 |||||
 Db 4 TTAATAAAAAAAG 18

Search completed: November 2, 2004, 12:50:35
 Job time : 3 secs

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108	15.2	1.1	21	1	BD023735	ACCESSION:BD023735	C 181	14.8	1.1	19	1	AR11970	ACCESSION:AR11970
109	15.2	1.1	25	1	AX117632	ACCESSION:AX117632	C 182	14.8	1.1	19	1	AR11483	ACCESSION:AR11483
C 110	15	1.1	17	1	AR187059	ACCESSION:AR187059	C 183	14.8	1.1	19	1	AR12484	ACCESSION:AR12484
C 111	15	1.1	17	1	AR187060	ACCESSION:AR187060	C 184	14.8	1.1	19	1	AR12485	ACCESSION:AR12485
C 112	15	1.1	17	1	AR323659	ACCESSION:AR323659	C 185	14.8	1.1	19	1	AR12486	ACCESSION:AR12486
C 113	15	1.1	17	1	AR323670	ACCESSION:AR323670	C 186	14.8	1.1	19	1	AR12487	ACCESSION:AR12487
C 114	15	1.1	17	1	AR323670	ACCESSION:AR323670	C 187	14.8	1.1	19	1	AR12488	ACCESSION:AR12488
C 115	15	1.1	17	1	AR323670	ACCESSION:AR323670	C 188	14.8	1.1	19	1	AR12489	ACCESSION:AR12489
C 116	15	1.1	17	1	AR323670	ACCESSION:AR323670	C 189	14.8	1.1	19	1	AR12490	ACCESSION:AR12490
C 117	15	1.1	19	1	AR102020	ACCESSION:AR102020	C 190	14.8	1.1	19	1	AR12485	ACCESSION:AR12485
C 118	15	1.1	19	1	AR134802	ACCESSION:AR134802	C 191	14.8	1.1	19	1	AR12486	ACCESSION:AR12486
C 119	15	1.1	19	1	AR352460	ACCESSION:AR352460	C 192	14.8	1.1	19	1	AR12487	ACCESSION:AR12487
C 120	15	1.1	20	1	E28098	ACCESSION:E28098	C 193	14.8	1.1	19	1	AR12488	ACCESSION:AR12488
C 121	15	1.1	20	1	AR294700	ACCESSION:AR294700	C 194	14.8	1.1	19	1	AR12489	ACCESSION:AR12489
C 122	15	1.1	20	1	AR307942	ACCESSION:AR307942	C 195	14.8	1.1	19	1	AR12490	ACCESSION:AR12490
C 123	15	1.1	20	1	AX048446	ACCESSION:AX048446	C 196	14.8	1.1	19	1	AR135293	ACCESSION:AR135293
C 124	15	1.1	21	1	AX804844	ACCESSION:AX804844	C 197	14.8	1.1	19	1	AR135294	ACCESSION:AR135294
C 125	15	1.1	21	1	AR034896	ACCESSION:AR034896	C 198	14.8	1.1	19	1	AR135295	ACCESSION:AR135295
C 126	14.8	1.1	18	1	AR034899	ACCESSION:AR034899	C 199	14.8	1.1	19	1	AR135296	ACCESSION:AR135296
C 127	14.8	1.1	18	1	AR058305	ACCESSION:AR058305	C 200	14.8	1.1	19	1	AR135297	ACCESSION:AR135297
C 128	14.8	1.1	18	1	AR097579	ACCESSION:AR097579	C 201	14.8	1.1	19	1	AR135298	ACCESSION:AR135298
C 129	14.8	1.1	18	1	AR101834	ACCESSION:AR101834	C 202	14.8	1.1	19	1	AR135302	ACCESSION:AR135302
C 130	14.8	1.1	18	1	AR106506	ACCESSION:AR106506	C 203	14.8	1.1	19	1	AR135304	ACCESSION:AR135304
C 131	14.8	1.1	18	1	AR106509	ACCESSION:AR106509	C 204	14.8	1.1	19	1	AR135305	ACCESSION:AR135305
C 132	14.8	1.1	18	1	BD222596	ACCESSION:BD222596	C 205	14.8	1.1	19	1	AR135315	ACCESSION:AR135315
C 133	14.8	1.1	18	1	E28535	ACCESSION:E28535	C 206	14.8	1.1	19	1	AR141898	ACCESSION:AR141898
C 134	14.8	1.1	18	1	E28536	ACCESSION:E28536	C 207	14.8	1.1	19	1	AR153863	ACCESSION:AR153863
C 135	14.8	1.1	18	1	179509	ACCESSION:179509	C 208	14.8	1.1	19	1	AR164173	ACCESSION:AR164173
C 136	14.8	1.1	18	1	AR196702	ACCESSION:AR196702	C 209	14.8	1.1	19	1	BD196900	ACCESSION:BD196900
C 137	14.8	1.1	18	1	AR196704	ACCESSION:AR196704	C 210	14.8	1.1	19	1	BD196911	ACCESSION:BD196911
C 138	14.8	1.1	18	1	AR215435	ACCESSION:AR215435	C 211	14.8	1.1	19	1	BD274438	ACCESSION:BD274438
C 139	14.8	1.1	18	1	AR222464	ACCESSION:AR222464	C 212	14.8	1.1	19	1	BD274439	ACCESSION:BD274439
C 140	14.8	1.1	18	1	AR412363	ACCESSION:AR412363	C 213	14.8	1.1	19	1	BD274440	ACCESSION:BD274440
C 141	14.8	1.1	18	1	AR473365	ACCESSION:AR473365	C 214	14.8	1.1	19	1	BD274441	ACCESSION:BD274441
C 142	14.8	1.1	18	1	AR487019	ACCESSION:AR487019	C 215	14.8	1.1	19	1	BD274449	ACCESSION:BD274449
C 143	14.8	1.1	18	1	AR487020	ACCESSION:AR487020	C 216	14.8	1.1	19	1	AR205798	ACCESSION:AR205798
C 144	14.8	1.1	18	1	AX004875	ACCESSION:AX004875	C 217	14.8	1.1	19	1	AR205799	ACCESSION:AR205799
C 145	14.8	1.1	18	1	AX004879	ACCESSION:AX004879	C 218	14.8	1.1	19	1	AR205800	ACCESSION:AR205800
C 146	14.8	1.1	18	1	AX008117	ACCESSION:AX008117	C 219	14.8	1.1	19	1	AR205801	ACCESSION:AR205801
C 147	14.8	1.1	18	1	AX008118	ACCESSION:AX008118	C 220	14.8	1.1	19	1	AR205809	ACCESSION:AR205809
C 148	14.8	1.1	18	1	AX008122	ACCESSION:AX008122	C 221	14.8	1.1	19	1	AR213490	ACCESSION:AR213490
C 149	14.8	1.1	18	1	AX008123	ACCESSION:AX008123	C 222	14.8	1.1	19	1	AR213491	ACCESSION:AR213491
C 150	14.8	1.1	18	1	AX028843	ACCESSION:AX028843	C 223	14.8	1.1	19	1	AR213492	ACCESSION:AR213492
C 151	14.8	1.1	18	1	AX047271	ACCESSION:AX047271	C 224	14.8	1.1	19	1	AR213493	ACCESSION:AR213493
C 152	14.8	1.1	18	1	AX047273	ACCESSION:AX047273	C 225	14.8	1.1	19	1	AR213494	ACCESSION:AR213494
C 153	14.8	1.1	18	1	AX104721	ACCESSION:AX104721	C 226	14.8	1.1	19	1	AR213495	ACCESSION:AR213495
C 154	14.8	1.1	18	1	AX104747	ACCESSION:AX104747	C 227	14.8	1.1	19	1	AR213496	ACCESSION:AR213496
C 155	14.8	1.1	18	1	AX105651	ACCESSION:AX105651	C 228	14.8	1.1	19	1	AR213497	ACCESSION:AR213497
C 156	14.8	1.1	18	1	AX108642	ACCESSION:AX108642	C 229	14.8	1.1	19	1	AR213501	ACCESSION:AR213501
C 157	14.8	1.1	18	1	AX268883	ACCESSION:AX268883	C 230	14.8	1.1	19	1	AR213502	ACCESSION:AR213502
C 158	14.8	1.1	18	1	AX355809	ACCESSION:AX355809	C 231	14.8	1.1	19	1	AR213503	ACCESSION:AR213503
C 159	14.8	1.1	18	1	AX547774	ACCESSION:AX547774	C 232	14.8	1.1	19	1	AR213512	ACCESSION:AR213512
C 160	14.8	1.1	18	1	AX547800	ACCESSION:AX547800	C 233	14.8	1.1	19	1	AR223465	ACCESSION:AR223465
C 161	14.8	1.1	18	1	AX814716	ACCESSION:AX814716	C 234	14.8	1.1	19	1	AR223463	ACCESSION:AR223463
C 162	14.8	1.1	18	1	AX814723	ACCESSION:AX814723	C 235	14.8	1.1	19	1	AR229557	ACCESSION:AR229557
C 163	14.8	1.1	18	1	AX814724	ACCESSION:AX814724	C 236	14.8	1.1	19	1	AR321589	ACCESSION:AR321589
C 164	14.8	1.1	18	1	AX814725	ACCESSION:AX814725	C 237	14.8	1.1	19	1	AR321590	ACCESSION:AR321590
C 165	14.8	1.1	18	1	AX814736	ACCESSION:AX814736	C 238	14.8	1.1	19	1	AR359805	ACCESSION:AR359805
C 166	14.8	1.1	18	1	BD085545	ACCESSION:BD085545	C 239	14.8	1.1	19	1	AR359806	ACCESSION:AR359806
C 167	14.8	1.1	19	1	A68209	ACCESSION:A68209	C 240	14.8	1.1	19	1	AR367447	ACCESSION:AR367447
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C 169	14.8	1.1	19	1	AR11371	ACCESSION:AR11371	C 242	14.8	1.1	19	1	AR399177	ACCESSION:AR399177
C 170	14.8	1.1	19	1	AR11946	ACCESSION:AR11946	C 243	14.8	1.1	19	1	AR403601	ACCESSION:AR403601
C 171	14.8	1.1	19	1	AR11947	ACCESSION:AR11947	C 244	14.8	1.1	19	1	AR403602	ACCESSION:AR403602
C 172	14.8	1.1	19	1	AR11948	ACCESSION:AR11948	C 245	14.8	1.1	19	1	AR403603	ACCESSION:AR403603
C 173	14.8	1.1	19	1	AR11949	ACCESSION:AR11949	C 246	14.8	1.1	19	1	AR403604	ACCESSION:AR403604
C 174	14.8	1.1	19	1	AR11950	ACCESSION:AR11950	C 247	14.8	1.1	19	1	AR403605	ACCESSION:AR403605
C 175	14.8	1.1	19	1	AR11951	ACCESSION:AR11951	C 248	14.8	1.1	19	1	AR403606	ACCESSION:AR403606
C 176	14.8	1.1	19	1	AR11952	ACCESSION:AR11952	C 249	14.8	1.1	19	1	AR403607	ACCESSION:AR403607
C 177	14.8	1.1	19	1	AR11953	ACCESSION:AR11953	C 250	14.8	1.1	19	1	AR403608	ACCESSION:AR403608
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C 179	14.8	1.1	19	1	AR11959	ACCESSION:AR11959	C 252	14.8	1.1	19	1	AR403613	ACCESSION:AR403613

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C 255	14.8	1.1	19	1	AR412338	ACCESSION:AR412338	C 328	14.8	1.1	20	1	AX547421	ACCESSION:AX547421
C 256	14.8	1.1	19	1	AR432616	ACCESSION:AR432616	C 329	14.8	1.1	20	1	AX556124	ACCESSION:AX556124
C 257	14.8	1.1	19	1	AR432617	ACCESSION:AR432617	C 330	14.8	1.1	20	1	AX556139	ACCESSION:AX556139
C 258	14.8	1.1	19	1	AR451262	ACCESSION:AR451262	C 331	14.8	1.1	20	1	AX664307	ACCESSION:AX664307
C 259	14.8	1.1	19	1	AR451282	ACCESSION:AR451282	C 332	14.8	1.1	20	1	AX664308	ACCESSION:AX664308
C 260	14.8	1.1	19	1	AX059378	ACCESSION:AX059378	C 333	14.8	1.1	20	1	AX708893	ACCESSION:AX708893
C 261	14.8	1.1	19	1	AX132398	ACCESSION:AX132398	C 334	14.8	1.1	20	1	AX741040	ACCESSION:AX741040
C 262	14.8	1.1	19	1	AX226133	ACCESSION:AX226133	C 335	14.8	1.1	20	1	AX741052	ACCESSION:AX741052
C 263	14.8	1.1	19	1	AX349249	ACCESSION:AX349249	C 336	14.8	1.1	20	1	BD008523	ACCESSION:BD008523
C 264	14.8	1.1	19	1	BD087505	ACCESSION:BD087505	C 337	14.8	1.1	20	1	BD080522	ACCESSION:BD080522
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C 304	14.8	1.1	20	1	AR488890	ACCESSION:AR488890	C 377	14.8	1.1	21	1	AX825146	ACCESSION:AX825146
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C 309	14.8	1.1	20	1	AX045779	ACCESSION:AX045779	C 382	14.8	1.1	21	1	AX825156	ACCESSION:AX825156
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ALIGNMENTS

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ACCESSION AX042782
VERSION AX042782.1 GI:11341390

LOCUS
AX042782
DEFINITION Sequence 348 from Patent WO0065088.
ACCESSION AX042782
VERSION AX042782.1 GI:11341390

KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Db 1 TTTTATTTTACAGACAGATCTT 25

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DEFINITION Sequence 10 from patent US 6395275.
ACCESSION AR370697
VERSION AR370697.1 GI:34607513
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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Unclassified.
1 (bases 1 to 25)
Barbas,C.F., Burton,D.R. and Lerner,R.A.
Synthetic human neutralizing monoclonal antibodies to human
immunodeficiency virus
Patent: US 6395275-A, 10 28-MAY-2002;
Location/Qualifiers
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DEFINITION Sequence 2755 from Patent WO0129262.
ACCESSION  AX117632
VERSION     AX117632.1. GI:14034583
KEYWORDS
SOURCE      .
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Picoult-Newburg, L. and Pohl, M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 2755 26-APR-2001;
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DEFINITION Sequence 5561 from Patent EP1281758.
ACCESSION  AX692829
VERSION     AX692829.1 GI:29415792
KEYWORDS
SOURCE      .
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5561 05-FEB-2003;
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ACCESSION  AX692830
VERSION     AX692830.1 GI:29415793
KEYWORDS
SOURCE      .
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5562 05-FEB-2003;
            Aeomica, Inc. (US)
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DEFINITION Sequence 5563 from Patent EP1281758.
ACCESSION  AX692831
VERSION     AX692831.1 GI:29415794
KEYWORDS
SOURCE      .
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5563 05-FEB-2003;
            Aeomica, Inc. (US)
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Qy      1306 TTTTATTTTTCAGACACAGA 1328
Db      1 TTTTCTTTTCTTTTGAAGAC 23

RESULT 7
AX825106/c
LOCUS      AX825106      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION  AX825106
VERSION     AX825106.1 GI:39750835
KEYWORDS
```

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1517 ATTAATAAATAAAGTAAAA 1537
DB 21 ATTAATAAATAAATAAATAA 1

RESULT 8
AR431307/c AR431307 24 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1 from patent US 6651008.
ACCESSION AR431307
VERSION AR431307.1 GI:40193275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Valsberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
TITLE Database system including computer code for predictive cellular
bioinformatics
JOURNAL Patent: US 6651008-A 1 18-NOV-2003;
location/Qualifiers

FEATURES
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1516 AATTAAAAAATAAGTAAAA 1537
DB 24 AATTAAAAAATAAGTAAAA 3

RESULT 9
AR253000/c AR253000 21 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 100 from patent US 6479236.
DEFINITION AR253000
ACCESSION AR253000
VERSION AR253000.1 GI:27301349
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Penny, L. and Galvin, M.
TITLE Genotyping the human UDP-glucuronosyltransferase 1 (UGT1) gene
JOURNAL Patent: US 6479236-A 100 12-NOV-2002;
location/Qualifiers

FEATURES
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 344 CCGCGCCGCCCGCCGAGAG 363
DB 21 CCGAGCACCGCCCGCAGAG 2

RESULT 10
AX825103/c AX825103 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 1 from Patent WO03072818.
DEFINITION AX825103
ACCESSION AX825103
VERSION AX825103.1 GI:39750832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 1 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
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Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.2%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAAGTAAA 1537
|||||
DB 20 TTTAAAAAAAAGTAAA 1

RESULT 11

AX825104/c

LOCUS AX825104 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 2 from Patent WO03072818.
ACCESSION AX825104
VERSION AX825104.1 GI:39750833
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 2 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

misc_binding 1
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modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 9
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAAGTAAA 1537
|||||
DB 20 TTTAAAAAAAAGTAAA 1

RESULT 12

AX825105/c

LOCUS AX825105 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 3 from Patent WO03072818.
ACCESSION AX825105
VERSION AX825105.1 GI:39750834
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

JOURNAL Patent: WO 03072818-A 3 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1

/bound_moiety="Biotin"

modified_base 3

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

modified_base 6

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

modified_base 9

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

modified_base 12

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

modified_base 15

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

modified_base 18

/note="LNA-T (Locked Nucleic Acid) "

/mod_base=OTHER

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAAGTAAA 1537
|||||
DB 20 TTTAAAAAAAAGTAAA 1

RESULT 13

AX825151/c

LOCUS AX825151 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 49 from Patent WO03072818.
ACCESSION AX825151
VERSION AX825151.1 GI:39750880
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 49 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 6
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/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
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modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
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/mod_base=OTHER

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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
modified_base
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18
modified_base
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18
/mod_base=OTHER

Query Match
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1518 TTAATAAAAAAAAAAGTAAA 1537
Db 21 TTAATAAAAAAAAAAAAAAAAAA 2

RESULT 14
AR261539 24 bp DNA linear PAT 29-JAN-2003
LOCUS AR261539 Sequence 6 from patent US 6322971.
DEFINITION AR261539
ACCESSION AR261539.1 GI:28072607
VERSION AR261539.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chetverin,A.B. and Kramer,F.R.
TITLE Oligonucleotide arrays and their use for sorting, isolating,
sequencing, and manipulating nucleic acids
JOURNAL Patent: US 6322971-A 6 27-NOV-2001;
FEATURES
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 90.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1518 TTAATAAAAAAAAAAGTAAA 1537
Db 2 TTAATAAAAAAAAAAAAAAAAAA 21

RESULT 15
A01996 23 bp DNA linear PAT 21-MAY-1993
LOCUS A01996 Reverse complement.
DEFINITION A01996
ACCESSION A01996
VERSION A01996.1 GI:344528
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
ARTIFICIAL SEQUENCES.
AUTHORS Patent: WO 8404538-A 24 22-NOV-1984;
JOURNAL Location/Qualifiers
1..23
/organism="synthetic construct"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 82.6%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1248 TTGTTTGTGTTTATACAGAT 1270
Db 1 TTGTTTGTGTTTGTGTCGAT 23
```

```
RESULT 16
A06442 23 bp DNA linear PAT 21-MAY-1993
LOCUS A06442 Reverse complement, duplicate.
DEFINITION A06442
ACCESSION A06442.1 GI:411262
VERSION A06442.1
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
ARTIFICIAL SEQUENCES.
AUTHORS Edens,L., Russell,S.W., Visser,C. and Vertrips,C.T.
TITLE Improvements in the expression of newly introduced genes in yeast
cells
JOURNAL Patent: EP 0129268-A 25 27-DEC-1984;
UNILEVER NV; UNILEVER PLC
FEATURES
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 82.6%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1248 TTGTTTGTGTTTATACAGAT 1270
Db 1 TTGTTTGTGTTTGTGTCGAT 23

RESULT 17
AR294636 19 bp DNA linear PAT 12-JUN-2003
LOCUS AR294636
DEFINITION AR294636 Sequence 6371 from patent US 6537751.
ACCESSION AR294636
VERSION AR294636.1 GI:31681920
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6371 25-MAR-2003;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1480 ATTCCAGCTATACATTAA 1497
Db 1 ATTCCAGCTACACATTAA 18

RESULT 18
AR084566 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084566/c
DEFINITION AR084566 Sequence 55 from patent US 5981185.
ACCESSION AR084566
VERSION AR084566.1 GI:10011337
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
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modified_base	18	/note="LNA-T (Locked Nucleic Acid) "	
		/mod_base=OTHER	
Query Match	1.2%;	Score 16.2;	DB 1; Length 21;
Best Local Similarity	85.7%;	Pred. No. 76;	
Matches	18;	Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1517	ATTAAAAAAAAAAAAAAAAAGTAAAA	1517
Db	21	AGTAAAAAAAAAAAAAAAAAAAAA	1
RESULT 28			
AX825114/c		21 bp	DNA
LOCUS			linear
DEFINITION	Sequence 12 from Patent WO03072818.		PAT 11-DEC-2003
AX825114			
ACCESSION	AX825114		
VERSION	AX825114.1		GI:39750843
KEYWORDS			
SOURCE			
ORGANISM			
			synthetic construct
			synthetic construct
			artificial sequences.
REFERENCE			
AUTHORS	1		Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE			Method for sorting single-stranded nucleic acids
JOURNAL			Patent: WO 03072818-A 12 04-SEP-2003;
			Degussa Bioactives GmbH (DE)
FEATURES			
source			location/Qualifiers
			1..21
			/organism="synthetic construct"
			/mol_type="unassigned DNA"
			/db_xref="taxon:32630"
			/note="Beschreibung der kuenstlichen
			Sequenz:Capture-Oligonukleotid"
			1
			/bound_molecy="Biotin"
			3
			/note="LNA-T (Locked Nucleic Acid) "
			/mod_base=OTHER
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			/note="LNA-T (Locked Nucleic Acid) "
			/mod_base=OTHER
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			/note="LNA-T (Locked Nucleic Acid) "
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			/mod_base=OTHER
			18
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			1.2%;
			Score 16.2;
			DB 1; Length 21;
			Best Local Similarity
			85.7%;
			Pred. No. 76;
			Matches
			18; Conservative
			0; Mismatches 3; Indels
			0; Gaps
			0;
QY	1517	ATTAAAAAAAAAAAAAAAAAGTAAAA	1517
Db	21	AGTAAAAAAAAAAAAAAAAAAAAA	1
RESULT 29			
AX825118/c		21 bp	DNA
LOCUS			linear
DEFINITION	Sequence 16 from Patent WO03072818.		PAT 11-DEC-2003
AX825118			
ACCESSION	AX825118		GI:39750847
VERSION	AX825118.1		GI:39750847
KEYWORDS			
SOURCE			
			synthetic construct

```

ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE       Method for sorting single-stranded nucleic acids
JOURNML     Patent: WO 03072818-A 16 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES
  source
      1..21
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          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="Beschreibung der kuenstlichen
          Sequenz: Capture-Oligonukleotid"
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          /bound_molecly="Biotin"
      3
          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
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          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
      9
          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
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          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
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          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
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          /mod_base=OTHER

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1516 AATTAAAAAAGTAA 1536
Db      21 AATAAAAAAGTAA 1

RESULT 30
AX825122/c
LOCUS      AX825122      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 20 from Patent WO03072818.
ACCESSION  AX825122
VERSION     AX825122.1 GI:39750851
KEYWORDS
SOURCE      .
            synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE       Method for sorting single-stranded nucleic acids
JOURNML     Patent: WO 03072818-A 20 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES
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          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="Beschreibung der kuenstlichen
          Sequenz: Capture-Oligonukleotid"
      1
          /bound_molecly="Biotin"
      3
          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER
      6
          /note="LNA-T (Locked Nucleic Acid)"
          /mod_base=OTHER

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PF 30-MAY-2000 JP 2000160324
PI KAO RI SHIMADA
PC C1201/68 C12N15/09 G01N33/50 C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
FH Key source Location/Qualifiers
FT source 1.22
/organism="Homo sapiens (human)".
location/Qualifiers
1.22
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

FEATURES
source

Query Match 1.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1517 ATTAAAAAAGTAAAA 1537
Db 2 ATCAAAAAAAAAAAAAAA 22

RESULT 34
ARJ15696/c ARJ15696 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 6233 from patent US 6559294.
DEFINITION ARJ15696
ACCESSION ARJ15696
VERSION ARJ15696.1 GI:31709122
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths, R., Hoiseeth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6233 06-MAY-2003;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1109 TTCATTTTCCCCC 1124
Db 17 TTCATTTTCCCCC 2

RESULT 35
A40126 A40126 20 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 2 from Patent WO9423026.
DEFINITION A40126
ACCESSION A40126
VERSION A40126.1 GI:2296284
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Vasseur, M., Blumentfeld, M., Megueni, S. and Poddevin, B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND APPLICATIONS
JOURNAL Patent: WO 9423026-A 2 13-OCT-1994;
COMMENT GENSET (FR)
Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES Location/Qualifiers
source 1.20
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;

OY 1520 AAAAAAAAAAAGTAAAG 1538
Db 1 AAAAAAAAAAAGCAAG 19

RESULT 36
ARJ39961/c ARJ39961 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207417.
DEFINITION ARJ39961
ACCESSION ARJ39961
VERSION ARJ39961.1 GI:14482457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;

OY 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 37
ARJ40280/c ARJ40280 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207454.
DEFINITION ARJ40280
ACCESSION ARJ40280
VERSION ARJ40280.1 GI:14482776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;

OY 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 38
ARJ40558/c ARJ40558 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207802.

ACCESSION ARI40558
VERSION ARI40558.1 GI:14483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAATAAAAAAAAAAGTAAAA 1537
Db 19 TAAATAAAAAAAAAAAAAA 1
RESULT 39
ARI82885 20 bp DNA linear PAT 20-APR-2002
LOCUS ARI82885
DEFINITION Sequence 57 from patent US 6339068.
ACCESSION ARI82885
VERSION ARI82885.1 GI:20226092
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Schorr, J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 57 15-JAN-2002;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19
RESULT 40
AX104051 20 bp DNA linear PAT 30-APR-2001
LOCUS AX104051
DEFINITION Sequence 243 from Patent WO0122972.
ACCESSION AX104051
VERSION AX104051.1 GI:13920248
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 243 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 41
AX281587 20 bp DNA linear PAT 02-NOV-2001
LOCUS AX281587
DEFINITION Sequence 10 from Patent WO0177305.
ACCESSION AX281587
VERSION AX281587.1 GI:16608838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 10 18-OCT-2001;
Arexis AB (SE)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetically generated primer"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 423 AGTGGCGGCTGCGCGCGCG 441
Db 1 AGTGGCGGCTGCGCGCGCG 19

RESULT 42
AX355382 20 bp DNA linear PAT 06-FEB-2002
LOCUS AX355382
DEFINITION Sequence 410 from Patent WO0197843.
ACCESSION AX355382
VERSION AX355382.1 GI:18620050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 410 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 43
LOCUS AX547104 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 243 from Patent WO02053141.
ACCESSION AX547104
VERSION AX547104.1 GI:25812248
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Bratzler, R.L.
AUTHORS Inhibition of angiogenesis by nucleic acids
TITLE Patent: WO 02053141-A 243 11-JUL-2003;
JOURNAL Coley Pharmaceutical Corp., Inc. (US)
FEATURES
SOURCE
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 44
LOCUS BD069976 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unmethylated CpG dinucleotide in the treatment of LPS-associated disorders.
ACCESSION BD069976
VERSION BD069976
KEYWORDS JP 2001513776-A/65.
SOURCE
ORGANISM
synthetic construct
artificial construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Schwartz, D.A. and Krieg, A.M.
TITLE Use of nucleic acids containing unmethylated CpG dinucleotide in the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 65 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
FEATURES
SOURCE
OS Artificial Sequence
PN JP 2001513776-A/65
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PI 28-FEB-1997 US 60/039405
PC DAVID A SCHWARTZ, ARTHUR M KRIEG
CC A61K49/00, C07H21/02, C07H21/04, A01N43/04
FH synthetic oligonucleotide
Key Location/Qualifiers
FT source
1. .20
/organism="Artificial Sequence".
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 45
LOCUS AR084563/c 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 52 from patent US 5981185.
ACCESSION AR084563
VERSION AR084563.1 GI:10011334
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Matsun, R.S., Coassan, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 52 09-NOV-1999;
FEATURES
SOURCE
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 20 GCGCGCGCGCGCGCGCGCG 2

RESULT 46
LOCUS AR084567 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 56 from patent US 5981185.
ACCESSION AR084567
VERSION AR084567.1 GI:10011338
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Matsun, R.S., Coassan, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 56 09-NOV-1999;
FEATURES
SOURCE
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 2 GCGCGCGCGCGCGCGCGCG 20

RESULT 47
LOCUS C0830490/c 21 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 2 from Patent WO200405153.
ACCESSION C0830490
VERSION C0830490.1 GI:50250830
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Schluesener, H. and Wendel, H.P.
AUTHORS Devices coated with substances that mediate the adhesion of biological material
TITLE Patent: WO 200405153-A 2 01-JUL-2004;
JOURNAL Eberhard-Karls-Universitaet Tuebingen (DE)

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FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Nukleotidsequenz"

Query Match
  1.1%: Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
  426 GCGCGCTGCGCGCGCGCG 444
  |||||
  20 GCGCGCGCGCGCGCGCGCG 2

RESULT 48
LOCUS
  CO830492
DEFINITION
  Sequence 4 from Patent WO2004055153.
ACCESSION
  CO830492.1 GI:50250832
KEYWORDS
  SOURCE
    synthetic construct
    artificial sequence.
REFERENCE
  1 Schluesener,H. and Wendel,H.P.
  Devices coated with substances that mediate the adhesion of
  biological material
  Patent: WO 2004055153-A 4 01-JUL-2004;
  Eberhard-Karls-Universitaet Tuebingen (DE)
  Location/Qualifiers
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Nukleotidsequenz"

FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Nukleotidsequenz"

Query Match
  1.1%: Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
  426 GCGCGCTGCGCGCGCGCG 444
  |||||
  2 GCGCGCGCGCGCGCGCGCG 20

RESULT 49
LOCUS
  AR242257
DEFINITION
  Sequence 20 from patent US 6472173.
ACCESSION
  AR242257
VERSION
  AR242257.1 GI:27288080
KEYWORDS
  SOURCE
    Unknown.
    ORGANISM
      Unknown.
      UNCLASSIFIED.
REFERENCE
  1 (bases 1 to 21)
  Ford,J. and Yeung,G.
  Chemokine receptor obtained from a cDNA library of fetal
  liver-spleen
  Patent: US 6472173-A 20 29-OCT-2002;
  Location/Qualifiers
    1. .21
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  1.1%: Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
  569 CAGCAGGCGCGCGCTAGG 587
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Db
  |||||
  1 CAGCAGGCTGCGCGTAGG 19

RESULT 50
LOCUS
  AR242262/c
DEFINITION
  Sequence 25 from patent US 6472173.
ACCESSION
  AR242262
VERSION
  AR242262.1 GI:27288085
KEYWORDS
  SOURCE
    Unknown.
    ORGANISM
      Unknown.
      UNCLASSIFIED.
REFERENCE
  1 (bases 1 to 21)
  Ford,J. and Yeung,G.
  Chemokine receptor obtained from a cDNA library of fetal
  liver-spleen
  Patent: US 6472173-A 25 29-OCT-2002;
  Location/Qualifiers
    1. .21
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  1.1%: Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
  569 CAGCAGGCGCGCGCTAGG 587
  |||||
  21 CAGCAGGCTGCGCGTAGG 3

RESULT 51
LOCUS
  AX825107/c
DEFINITION
  Sequence 5 from Patent WO03072818.
ACCESSION
  AX825107
VERSION
  AX825107.1 GI:39750836
KEYWORDS
  SOURCE
    synthetic construct
    artificial sequence.
ORGANISM
  REFERENCE
    1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
    Method for sorting single-stranded nucleic acids
    Patent: WO 03072818-A 5 04-SEP-2003;
    Degussa Bioactives GmbH (DE)
  JOURNAL
    Location/Qualifiers
      1. .21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kueneftlichen
        Sequenz:capture-Oligonukleotid"

FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Beschreibung der kueneftlichen
      Sequenz:capture-Oligonukleotid"

misc_binding
  1 /bound_moiety="Biotin"
modified_base
  3 /note="LNA-T (Locked Nucleic Acid)"
modified_base
  6 /note="LNA-T (Locked Nucleic Acid)"
modified_base
  9 /note="LNA-T (Locked Nucleic Acid)"
modified_base
  12 /note="LNA-T (Locked Nucleic Acid)"
modified_base
  15 /note="LNA-T (Locked Nucleic Acid)"
modified_base
  18 /note="LNA-T (Locked Nucleic Acid)"
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 52
AX825108/c AX825108 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 6 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/misc_binding
1 /bound_molecly="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
modified_base
6 /mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
modified_base
12 /mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
modified_base
18 /mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 53
AX825109/c AX825109 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION AX825109.1 GI:39750838
KEYWORDS
SOURCE
ORGANISM
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artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 7 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/misc_binding
1 /bound_molecly="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
modified_base
6 /mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
modified_base
12 /mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
modified_base
18 /mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 54
AX825111/c AX825111 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 9 from Patent WO03072818.
ACCESSION AX825111
VERSION AX825111.1 GI:39750840
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 9 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/misc_binding
1 /bound_molecly="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
modified_base
6 /mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 55
AX825112/c AX825112 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 10 from Patent WO03072818.
DEFINITION AX825112
ACCESSION AX825112
VERSION AX825112.1 GI:39750841
KEYWORDS

SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 10 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES
source Location/Qualifiers

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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/mod_molecly="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

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RESULT 56
AX825113/c AX825113 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 11 from Patent WO03072818.
DEFINITION AX825113
ACCESSION AX825113
VERSION AX825113.1 GI:39750842
KEYWORDS
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SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 11 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES
source Location/Qualifiers

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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/mod_molecly="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 57
AX825115/c AX825115 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 13 from Patent WO03072818.
DEFINITION AX825115
ACCESSION AX825115
VERSION AX825115.1 GI:39750844
KEYWORDS

SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 13 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES
source Location/Qualifiers

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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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misc_binding      /note="Beschreibung der kuenstlichen
                  Sequenz:Capture-Oligonukleotid"
                  1
modified_base     /bound_molecy="Biotin"
                  3
modified_base     /note="LNA-T (Locked Nucleic Acid)"
                  6
modified_base     /mod_base=OTHER
                  9
modified_base     /note="LNA-T (Locked Nucleic Acid)"
                  12
modified_base     /mod_base=OTHER
                  15
modified_base     /note="LNA-T (Locked Nucleic Acid)"
                  18
modified_base     /mod_base=OTHER

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY              1519 TAAAAAAGTAAA 1537
Db              19 TAAAAAAAAAAAAA 1

RESULT 58
AX825116/c      AX825116      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS           AX825116
DEFINITION      Sequence 14 from Patent WO03072818.
ACCESSION       AX825116
VERSION         AX825116.1 GI:39750845
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE       1
AUTHORS         Boekamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE           Method for sorting single-stranded nucleic acids
JOURNAL         Patent: WO 03072818-A 14 04-SPP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES        Location/Qualifiers
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:33630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
                1
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                18
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Query Match	1.1%;	Score 15.8;	DB 1;	Length 21;
Best Local Similarity	89.5%;	Pred. No. 97;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1519	TAAGAAAAAGTAA	1537	
Db	19	TAAGAAAAAGTAA	1	
RESULT 59				
AX825117/c				
LOCUS	AX825117	21 bp	DNA	linear
DEFINITION	Sequence 15 from Patent WO03072818.			PAT 11-DEC-2003
ACCESSION	AX825117			
VERSION	AX825117.1	GI:39750846		
KEYWORDS				
SOURCE				
ORGANISM	synthetic construct			
REFERENCE	1			
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 15 04-SEP-2003;			
DEGUS	Degussa Bioactives GmbH (DE)			
LOCATION	Qualifiers			
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	/db_xref="taxon:32630"			
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	Sequenz: Capture-Oligonukleotid"			
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	3			
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	modified_base			

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REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 50 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
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  modified_base
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  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAAAGTAAA 1537
Db 20 TAAAAAAAAAAAAAAAAA 2

RESULT 61
AX825153/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825153
DEFINITION Sequence 51 from Patent WO03072818.
ACCESSION AX825153
VERSION AX825153.1 GI:39750862
KEYWORDS
SOURCE
  .
  synthetic construct
  synthetic construct
  artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 51 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
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    /db_xref="taxon:32630"
    /note="Beschreibung der kuenstlichen
    Sequenz:Capture-Oligonukleotid"
  misc_binding
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  modified_base
    3
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  modified_base
    6
    /mod_base=OTHER
  modified_base
    9
    /note="LNA-T (Locked Nucleic Acid)"
  modified_base
    12
    /note="LNA-T (Locked Nucleic Acid)"
  modified_base
    15
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  modified_base
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    /mod_base=OTHER
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  modified_base
    15
    /note="LNA-T (Locked Nucleic Acid)"
  modified_base
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  modified_base
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Query Match
  1.1%; Score 15.8; DB 1; Length 21;
  Best Local Similarity 89.5%; Pred. No. 97;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAAAGTAAA 1537
Db 21 TAAAAAAAAAAAAAAAAA 3

RESULT 62
AX825153/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825153
DEFINITION Sequence 61 from Patent WO03072818.
ACCESSION AX825153
VERSION AX825153.1 GI:39750892
KEYWORDS
SOURCE
  .
  synthetic construct
  synthetic construct
  artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 61 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
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    /db_xref="taxon:32630"
    /note="Beschreibung der kuenstlichen
    Sequenz:Capture-Oligonukleotid"
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  modified_base
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  modified_base
    6
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RESULT 63
LOCUS AX58499 22 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 415 from Patent WO03000928.
ACCESSION AX58499
VERSION AX58499.1 GI:29160856
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
Peterson,M.W. and Bigner,H.I.
TITLE Methods for identification of cancer cell surface molecules and
cancer specific promoters, and therapeutic uses thereof
JOURNAL Patent: WO 0300928-A 415 03-JAN-2003;
Odin Medical A/S (DK)
FEATURES
Source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 89.5%; Pred. NO. 93;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 989 GTTCTGTTCTGTGAGAA 1007
DB 2 GTTCTGTCTGTGAGAA 20
RESULT 64
LOCUS AR164336 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 19 from patent US 6271369.
ACCESSION AR164336
VERSION AR164336.1 GI:16235464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
JOURNAL Chimeric molecules targeted to viral RNAs
DEFINITION Patent: US 6271369-A 19 07-AUG-2001;
FEATURES
Source Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 22
RESULT 65
LOCUS I31828 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5583032.
ACCESSION I31828
VERSION I31828.1 GI:1822619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.

TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 19 10-DEC-1996;
FEATURES
Source Location/Qualifiers
1..22
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/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 22
RESULT 66
LOCUS I69425 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 19 from patent US 5677289.
ACCESSION I69425
VERSION I69425.1 GI:2831547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
JOURNAL Method of cleaving specific strands of RNA and medical treatments
DEFINITION Patent: US 5677289-A 19 14-OCT-1997;
FEATURES
Source Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 22
RESULT 67
LOCUS BD254424 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254424
VERSION BD254424.1 GI:33064194
KEYWORDS JP 2002541795-A/2217.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 17)
TITLE Blatt,L., Zwick,M., Pavco,P. and Mcswigen,J.
JOURNAL Regulation of repressor genes using nucleic acid molecules
DEFINITION Patent: JP 2002541795-A 2217 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2217
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02/A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,

PC (C12N5/00,C12N1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
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/organism='Eukaryote'.
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 646 GCCGTGCCGAGCCGCC 662
DB 17 GCCGGCCGAGCCGCC 1

RESULT 68
LOCUS AR187058 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2546 from patent US 6346398.
ACCESSION AR187058
VERSION AR187058.1 GI:20233023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2546 12-FEB-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAAGTAGA 1

RESULT 69
LOCUS AR286187 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 559 from patent US 6528640.
ACCESSION AR286187
VERSION AR286187.1 GI:29723783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 559 04-MAR-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1248 TTGTGTTGTTTTTAA 1264
DB 1 TTGTGTTGTTTTTAA 17

RESULT 70
LOCUS AR323668/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1070 from patent US 6566127.
ACCESSION AR323668
VERSION AR323668.1 GI:33709476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1070 20-MAY-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAAGTAGA 1

RESULT 71
LOCUS AR398177 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 558 from patent US 6617438.
ACCESSION AR398177
VERSION AR398177.1 GI:40135776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 558 09-SEP-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1248 TTGTGTTGTTTTTAA 1264
DB 1 TTGTGTTGTTTTTAA 17

RESULT 72
LOCUS AX804693 18 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 861 from Patent WO03060160.
ACCESSION AX804693
VERSION AX804693.1 GI:38521834
KEYWORDS
SOURCE Oreoehromis niloticus (Nile tilapia)
ORGANISM Oreoehromis niloticus; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genomae ASA (NO)
Patent: WO 03060160-A 861 24-JUL-2003;
Location/Qualifiers

FEATURES
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1..18
/organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"

Query Match 1.1%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 660 GCCTCAGACTCAGCTCT 676
DB 1 GCCTCAGCTCAGCTCT 17

RESULT 73
A88305
LOCUS A88305 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 453 from Patent WO9833904.
ACCESSION A88305
VERSION A88305.1 GI:6736875
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 453 06-AUG-1998;
BIOGOSTIK GBS (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers

FEATURES
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1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 4 AAAACAAAAAAGTAAA 20

RESULT 74
A90272
LOCUS A90272 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 453 from Patent EP0856579.
ACCESSION A90272
VERSION A90272.1 GI:6738786
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 453 05-AUG-1998;
BIOGOSTIK GBS (DE)
Location/Qualifiers

FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"

/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 4 AAAACAAAAAAGTAAA 20

RESULT 75
AX356277
LOCUS AX356277 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 71 from Patent WO200905.
ACCESSION AX356277
VERSION AX356277.1 GI:18620784
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Comner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
Plant regulatory sequences for selective control of gene expression
Patent: WO 0200905-A 71 03-JAN-2002;
Monsanto Technology LLC (US)
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 552 GCGTGTGCGTGGCTTCG 568
DB 2 GCGAGTGGTGGCTTCG 18

RESULT 76
BD065818
LOCUS BD065818 20 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065818
VERSION BD065818.1 GI:22611421
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
Schlingensiepen,K.H. and Brysch,W.
An antisense oligonucleotide preparation method
Patent: JP 2001511000-A 453 07-AUG-2001;
BIOGOSTIK GEBELTSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/453
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTTAA 1536
|||||
4 AAAAAAAGTTAA 20

RESULT 77
AX118267/c AX118267 21 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 3390 from Patent WO0129262.
DEFINITION AX118267
ACCESSION AX118267
VERSION AX118267.1 GI:14035218
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3390 26-APR-2001;
Orchid Biosciences, Inc. (US)
LOCATION/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GTGTCAAGATAGGTT 1419
|||||
21 GTGTCAAGATAGGTT 5

RESULT 78
AR092032/c AR092032 20 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 56 from patent US 5998141.
DEFINITION AR092032
ACCESSION AR092032
VERSION AR092032.1 GI:10018786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. Laurene.
TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 5998141-A 56 07-DEC-1999;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTTAA 1056
|||||
20 GTGGCGCGCGGTGTGTTAA 1

RESULT 79
AR112167/c AR112167 20 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 56 from patent US 6130041.
DEFINITION

ACCESSION AR112167
VERSION AR112167.1 GI:14092067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. Laurene.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 56 10-OCT-2000;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTTAA 1056
|||||
20 GTGGCGCGCGGTGTGTTAA 1

RESULT 80
AR149209/c AR149209 20 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 56 from patent US 6228581.
DEFINITION AR149209
ACCESSION AR149209
VERSION AR149209.1 GI:15113800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. L. and Ordovas, J. M.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6228581-A 56 08-MAY-2001;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTTAA 1056
|||||
20 GTGGCGCGCGGTGTGTTAA 1

RESULT 81
BD229218 BD229218 20 bp DNA linear PAT 17-JUL-2003
LOCUS Genotype determination of human UDP-glucuronosyl transferase 2B4 (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes.
DEFINITION BD229218
ACCESSION BD229218.1 GI:33038988
VERSION BD229218.1
KEYWORDS JP 2002521067-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Galvin, M., Miller, A., Penny, L. and Riechy, M.
TITLE Genotype determination of human UDP-glucuronosyl transferase 2B4 (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
JOURNAL Patent: JP 2002521067-A 90 16-JUL-2002;
AXIS PHARMACEUTICALS INC
OS Homo sapiens (human)

PN JP 2002521067-A/90
PD 16-JUL-2002
PR 22-JUL-1999 JP 2000562558
PI 28-JUL-1998 US 60/094391
PI MARKER GALVIN, ANDREW MILLER, LAURA PENNY, MICHAEL RIEDY PC
C12N15/09, C12N15/00, C12Q1/69, C12N15/00, C12N15/00 CC
Genotype determination of human UDP-glucuronosyl transferase
284 (UGT2B4),
CC 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
FH key Location/Qualifiers
FT source 1..20
/organism="Homo sapiens (human)"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1632 CCTCCCTACCTTTGAAAA 1651
Db 1 CCTGGCTACACTTTGAAAA 20

RESULT 82
AR309844 AR309844 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR309844
DEFINITION Sequence 4 from patent US 6555670.
ACCESSION AR309844
VERSION AR309844.1 GI:31701953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Aizawa, A., Kawakami, A. and Kondo, T.
TITLE Testis-specific gene
JOURNAL Patent: US 6555670-A 4 29-APR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1300 AATCTATTTTATTTTC 1319
Db 1 AAGCTTTTATTTTTC 20

RESULT 83
AR349470 AR349470 20 bp DNA linear PAT 17-AUG-2003
LOCUS AR349470
DEFINITION Sequence 92 from patent US 6586175.
ACCESSION AR349470
VERSION AR349470.1 GI:33750263
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Galvin, M., Miller, A., Penny, L. and Riedy, M.
TITLE Genotyping the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene
JOURNAL Patent: US 6586175-A 92 01-JUL-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1632 CCTCCCTACCTTTGAAAA 1651
Db 1 CCTGGCTACACTTTGAAAA 20

RESULT 84
AX298541/c AX298541/c 20 bp DNA linear PAT 26-NOV-2001
LOCUS AX298541/c
DEFINITION Sequence 175 from Patent WO0183749.
ACCESSION AX298541
VERSION AX298541.1 GI:17128531
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,
Li, X., Ohmen, J.D., Reed, D.R., Ross, B., and Tordoff, M.G.
Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
Patent: WO 0183749-A 175 08-NOV-2001;
JOURNAL WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)

FEATURES
source 1..20
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 808 CTGAATTTGTGTGTCATC 827
Db 20 CGAATTTGTGTGTCATC 1

RESULT 85
AX404077 AX404077 20 bp DNA linear PAT 14-JUN-2002
LOCUS AX404077
DEFINITION Sequence 4 from Patent EP1195382.
ACCESSION AX404077
VERSION AX404077.1 GI:21437393
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Aizawa, A., Kawakami, A. and Kondo, T.
TITLE Testis-specific gene
JOURNAL Patent: EP 1195382-A 4 10-APR-2002;
LIVESTOCK IMPROVEMENT ASSOCIATION of Japan, Inc. (JP) ; President
of Gunma University (JP)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1300 AATCTATTTTATTTTC 1319
Db 1 AAGCTTTTATTTTTC 20

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RESULT 86
AX488408
LOCUS AX488408 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 5708 from Patent WO02053728.
ACCESSION AX488408
VERSION AX488408.1 GI:22322488
KEYWORDS
SOURCE
ORGANISM
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales;
REFERENCE
1 Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 5708 11-JUL-2002;
Eliara Pharmaceuticals, Inc. (US)
FEATURES
source
1..20
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 727 GCTGTGCTGCTGCTTGT 746
Db 1 GCTCTCTCTCTGCTGTTGT 20

RESULT 87
AX770111
LOCUS AX770111 20 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 9 from Patent WO03016562.
ACCESSION AX770111
VERSION AX770111.1 GI:32437689
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Glacquel,B.
TITLE Compositions and methods for detecting multidrug resistant strains
JOURNAL of M. tuberculosis having mutations in genes of the mutR family
INSTITUT PASTEUR (FR)
FEATURES
source
1..20
/location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 439 CCGGCGACGATCCCGGCT 458
Db 1 CCGGCGACGATCCCTCGTT 20

RESULT 88
BD143136
LOCUS BD143136 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel testis-specific gene.
ACCESSION BD143136
VERSION BD143136.1 GI:27848894
KEYWORDS
SOURCE
synthetic construct
```

```
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Aizawa,A., Kawakami,A. and Kondo,T.
TITLE Novel testis-specific gene
JOURNAL Patent: JP 2002112777-A 3 16-APR-2002;
KACHIKU KAIryo JIGYODAN, PRESIDENT OF GUNMA UNIVERSITY
COMMENT
OS Artificial Sequence
PN JP 2002112777-A/3
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303994
PI AKIRA AIZAWA, AKIKO KAWAKAMI, TOSHITAKO KONDO
PC C12N15/09; C07K14/47; C12N15/00
CC Novel testis-specific gene
FH Key
FT source
1..20
/location/Qualifiers
/organism="Artificial Sequence".
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1300 AATCTATTTTTTAAATTTT 1319
Db 1 AAGCTTTTTTTTTTTTTTTC 20

RESULT 89
AX825106
LOCUS AX825106 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION AX825106
VERSION AX825106.1 GI:39750835
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 4 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base
5
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1246 TCTTGTGTTGTTTAT 1265
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TTTTGTGTTTGTAT 21

RESULT 90
A20525 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SA216.
DEFINITION A20525
VERSION A20525.1 GI:583360
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 22 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 GCGCGCGCGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GCGCGCGCGCGCGAGTGC 21

RESULT 91
A20526 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SA216.
DEFINITION A20526
VERSION A20526.1 GI:579020
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 23 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 GCGCGCGCGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCGCGCGCGCGAGTGC 1

RESULT 92
A20531 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SAT216.
DEFINITION

ACCESSION A20531
VERSION A20531.1 GI:583363
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 28 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 GCGCGCGCGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GCGCGCGCGCGTGCAGTGC 21

RESULT 93
A20532 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SAT216.
DEFINITION A20532
VERSION A20532.1 GI:579023
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 29 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 597 GCGCGCGCGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCGCGCGCGCGTGCAGTGC 1

RESULT 94
A20532 21 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 11 from patent US 6204435.
DEFINITION A20532
VERSION A20532.1 GI:15104912
KEYWORDS
SOURCE . Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Felteison, J.S., Schepf, H.E., Narva, K.E., Stockhoff, B.A.,
Schmelts, J., Loewer, D., Dullum, C., Joseph, J., Muller-Cohn, J. and
Stamp, L.M.
TITLE Pesticidal toxins and nucleotide sequences which encode these
toxins
JOURNAL Patent: US 6204435-A 11 20-MAR-2001;
FEATURES
source 1..21

		/organism="unknown"			
		/mol_type="unassigned DNA"			
Query Match	1.1%;	Score 15.2;	DB 1;	Length 21;	
Best Local Similarity	85.0%;	Pred. No. 1.4e+02;			
Matches 17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
OY	1630	ATCCTCCCTACCCCTTTGAA	1649		
Db	2	ATCCTCCCTACACCTTCTAA	21		
RESULT 95					
LOCUS	ARI57200	21 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	Sequence 11 from patent US 6242669.				
ACCESSION	ARI57200				
VERSION	ARI57200.1	GI:15125904			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 21)				
	Fetters, J.S., Schnepf, H. Ernest., Narva, K.E., Stockhoff, B.A.,				
	Schmeltz, J., Loewer, D., Dullum, C., Joseph, Muller-Cohn, J., Stamp, L.,				
	Morrill, G., and Flinsrad, Lee, S.				
TITLE	Pesticidal toxins and nucleotide sequences which encode these toxins				
JOURNAL	Patent: US 6242669-A 11 05-JUN-2001;				
FEATURES	Location/Qualifiers				
source	1..21				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	1.1%;	Score 15.2;	DB 1;	Length 21;	
Best Local Similarity	85.0%;	Pred. No. 1.4e+02;			
Matches 17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
OY	1630	ATCCTCCCTACCCCTTTGAA	1649		
Db	2	ATCCTCCCTACACCTTCTAA	21		
RESULT 96					
LOCUS	E08187	21 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	Primer for isolation of the promoter in rice starch-branching enzyme.				
ACCESSION	E08187				
VERSION	E08187.1	GI:2176308			
KEYWORDS	JP 1994261767-A/5.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 21)				
AUTHORS	Baba, T., and Shimada, H.				
TITLE	NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE				
JOURNAL	Patent: JP 1994261767-A 5 20-SEP-1994;				
	MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK				
COMMENT	OS None				
	OC Artificial sequences.				
	PN JP 1994261767-A/5				
	PD 20-SEP-1994				
	PF 22-OCT-1993 JP 1993265171				
	PR 29-OCT-1992 JP 92P 291719				
	PI BABA TADASHI, SHIMADA HIROAKI				
	PC C12N15/54, A01H5/00, C12N5/10, C12P19/16//A23L1/10, C12N9/10, CC				
	strandedness: Single;				
	CC topology: linear;				
	FH Key				
	FH Location/Qualifiers				
FT	source 1..21				
	/organism='Artificial sequences'.				

FEATURES	Location/Qualifiers
source	1..21 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
Query Match	1.1%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred.No.1.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	546 GTGGTGCCTGTGCGTCGT 565 2 GTGTGTGGTGTCGCCGCGT 21
RESULT 97	
LOCUS	AR437180 21 bp DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 11 from patent US 6656908.
ACCESSION	AR437180
VERSION	AR437180.1 GI:40202037
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 21)
AUTHORS	Felteson,J.S., Schnepf,H.E., Narva,K.E., Stockhoff,B.A., Schmelts,J., Loewer,D., Bullum,C.J., Muller-Cohn,J., Stamp,L., Morrill,G. and Finstad-Lee,S. Pesticidal toxins and nucleotide sequences which encode these toxins
TITLE	Patent: US 6656908-A 11 02-DEC-2003; Location/Qualifiers
JOURNAL	1..21 /organism="unknown" /mol_type="genomic DNA"
FEATURES	
source	
Query Match	1.1%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred.No.1.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	1630 ATCCTCCCTACCCTTTGAA 1649 2 ATCCTCCCTACTTCTTA 21
Db	
RESULT 98	
LOCUS	AX825119 21 bp DNA linear PAT 11-DEC-2003
DEFINITION	Sequence 17 from Patent WO03072818.
ACCESSION	AX825119
VERSION	AX825119.1 GI:39750848
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818-A 17 04-SEP-2003; Degussa Bioactives GmbH (DE) Location/Qualifiers
JOURNAL	1..21 /organism="synthetic construct" /mol_type="unnassigned DNA" /db_xref="taxon:32630" /note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
FEATURES	1 /bound_motety="Biotin"
source	3 /note="LNA-T (Locked Nucleic Acid)" /mod_base=OTHER

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modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1518 TTTAAAAAAAGTAAAA 1537
Db 21 TTTCAAAAAAAAAAAAAA 2

RESULT 99
AX825120/c AX825120 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 18 from Patent WO03072818.
DEFINITION AX825120
ACCESSION AX825120
VERSION AX825120.1 GI:39750849
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNML Patent: WO 03072818-A 18 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
misc_binding 3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1518 TTTAAAAAAAGTAAAA 1537
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Db 20 TTTCAAAAAAAAAAAAAA 1

RESULT 100
AX825121/c AX825121 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 19 from Patent WO03072818.
DEFINITION AX825121
ACCESSION AX825121
VERSION AX825121.1 GI:39750850
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNML Patent: WO 03072818-A 19 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
misc_binding 3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
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Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1518 TTTAAAAAAAGTAAAA 1537
Db 20 TTTCAAAAAAAAAAAAAA 1

RESULT 101
AX825135/c AX825135 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 33 from Patent WO03072818.
DEFINITION AX825135
ACCESSION AX825135
VERSION AX825135.1 GI:39750864
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNML Patent: WO 03072818-A 33 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source 1..21
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Sequenz:Capture-Oligonukleotid"
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15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAGTAAAA 1537
|||
21 TTGAAAAAAAAAAAAA 2

RESULT 102
AX825136 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 34 from Patent WO03072818.
DEFINITION AX825136
ACCESSION AX825136.1 GI:39750865
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITL Method for sorting single-stranded nucleic acids
JOURN Patent: WO 03072818-A 34 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers
1..21
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Sequenz:Capture-Oligonukleotid"
misc_binding
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modified_base
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Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAGTAAAA 1537
|||
21 TTGAAAAAAAAAAAAA 2

RESULT 104
AX825137 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 35 from Patent WO03072818.
DEFINITION AX825137
ACCESSION AX825137.1 GI:39750866
VERSION
KEYWORDS
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/mod_base=OTHER

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1302 TCTATTTTATTTCAG 1321
|||
2 TTTTTCAG 21

RESULT 103
AX825136 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 34 from Patent WO03072818.
DEFINITION AX825136
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITL Method for sorting single-stranded nucleic acids
JOURN Patent: WO 03072818-A 34 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
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Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAGTAAAA 1537
|||
20 TTGAAAAAAAAAAAAA 1

RESULT 104
AX825137 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 35 from Patent WO03072818.
DEFINITION AX825137
ACCESSION AX825137.1 GI:39750866
VERSION
KEYWORDS
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SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	artificial sequences.			
AUTHORS	1			
TITLE	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.			
JOURNAL	Method for sorting single-stranded nucleic acids			
DEPOSIT	Patent: WO 03072818-A 35 04-SEP-2003;			
DEPOSIT	Degussa Bioactives GmbH (DE)			
LOCATION	location/Qualifiers			
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5.	Sequenz: Capture-Oligonukleotid"			
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24.	/note="LNA-T (Locked Nucleic Acid) "			
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Db	21	TGAAAAAAAAAAAAAAAAAAAAA	2
RESULT 107			
LOCUS	BD008680	21 bp	DNA linear
DEFINITION	Novel pesticidal toxins and nucleotide sequences which encode these toxins.		
ACCESSION	BD008680		
VERSION	BD008680.1	GI:18637053	
KEYWORDS	JP 2001502919-A/8.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Fetteison,J.S., Schnepf,E.H., Narva,K.E., Stockhoff,B.A., Schmeltz,J.L., Loewer,D., Schwab,G., Dullum,C.J., Cohn,J.M. and Stemp,L.		
TITLE	New pestictidal toxins and nucleotide sequences which encode these		
JOURNAL	toxins Patent: JP 2001502919-A 8 06-MAR-2001; MYCOGEN CORP OS Unidentified PN JP 2001502919-A/8 PD 06-MAR-2001 PF 30-OCT-1997 JP 1998520788		
COMMENT	PR JERALD S FETTELSON, ERNEST H SCHNEPF, KENNETH E NARVA, PI BRIAN A STOCKHOFF, PI JAMES L SCHMELTS, DAVID LOEWER, GEORGE SCHWAB, PI CHARLES JOSEPH DULLUM, PI JUDY MULLER COHN, LISA STRAMP PC C12N15/32, C07K14/325, C12Q1/68, A01N63/00, C12N15/82 CC Strandedness: Single; CC Topology: linear; FH Key Location/Qualifiers FT source 1..21 /organism='Unidentified', FT /location/Qualifiers		
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Query Match	1.1%;	Score 15.2;	DB 1; Length 21;
Best Local Similarity	85.0%;	Pred. No. 1.4e+02;	
Matches	17;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
OY	1630	ATCCTCCCTACCCTTTGCA	1649
Db	2	ATCCTCCCTACACTTCCTCA	21
RESULT 108			
LOCUS	BD023735	21 bp	DNA linear
DEFINITION	Beta-galactosidase having reversibly inactive lactase activity.		
ACCESSION	BD023735		
VERSION	BD023735.1	GI:32564958	
KEYWORDS	JP 2001506136-A/1.		
SOURCE	Eremothecium goessypii (Ashbya goessypii)		
ORGANISM	Eremothecium goessypii		
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium. 1 (bases 1 to 21)		
AUTHORS	Karatras,C.N., Turner,J.D., Eino,M., Kabel,J.J. and Amantea,G.F.		
TITLE	Beta-galactosidase having reversibly inactive lactase activity		
JOURNAL	Patent: JP 2001506136-A 1 15-MAY-2001; NEXIA BIOTECHNOLOGIES INC PN JP 2001506136-A/1 PD 15-MAY-2001 PF 29-DEC-1997 JP 1998529775 PR 31-DEC-1996 US 08/775842		
COMMENT			

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FEATURES
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            1..21
                /organism="Eremothecium goseypii"
                /mol_type="genomic DNA"
                /db_xref="taxon:33169"

Query Match
Best Local Similarity 85.0%; Pred. No. 1.4e+02; Length 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1605 GGTCCTCCGAGACTGCATAG 1624
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Ddb 1 GGTACCGAGCACTGGATGG 20

RESULT 109
AXI17632 25 bp DNA linear PAT 11-MAY-2002
DEFINITION Sequence 2755 from Patent WO0129262.
ACCESSION AXI17632
VERSION AXI17632.1 GI:14034583
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2755 26-APR-2001;
Orchid Biosciences, Inc. (US)
location/Qualifiers
FEATURES
    source
        1..25
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match
Best Local Similarity 85.0%; Pred. No. 1.2e+02; Length 25;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1511 CTGTTATTAAAAAAA 1530
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Ddb 5 CTTTAAAAAAAAAAAAA 24

RESULT 110
ARI87059/c 17 bp DNA linear PAT 20-APR-2002
LOCUS ARI87059
DEFINITION Sequence 2547 from patent US 6346398.
ACCESSION ARI87059
VERSION ARI87059.1 GI:20233024
KEYWORDS
SOURCE unknown.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.,MSWiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES
    location/Qualifiers
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

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Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTA 1534
Db 16 AAAAAAAAAAAGTA 2

RESULT 111
ARI87060/c ARI87060 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2548 from patent US 6346398.
ACCESSION ARI87060
VERSION ARI87060.1 GI:20233025
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTA 1534
Db 15 AAAAAAAAAAAGTA 1

RESULT 112
AR323669/c AR323669 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1071 from patent US 6566127.
ACCESSION AR323669
VERSION AR323669.1 GI:33709477
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTA 1534
Db 16 AAAAAAAAAAAGTA 2

RESULT 113
AR323670/c AR323670 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1072 from patent US 6566127.
ACCESSION AR323670
VERSION AR323670.1 GI:33709478

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTA 1534
Db 15 AAAAAAAAAAAGTA 1

RESULT 114
AX753821/c AX753821 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 168 from Patent WO03037931.
ACCESSION AX753821
VERSION AX753821.1 GI:32166518
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 168 08-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 726 TGCTGTGCTGCTGC 740
Db 17 TGCTGTGCTGCTGC 3

RESULT 115
AX753822/c AX753822 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 169 from Patent WO03037931.
ACCESSION AX753822
VERSION AX753822.1 GI:32166519
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 169 08-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
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Query Match
  1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 TGCTGTTGCTGCTGC 740
DB 16 TGCTGTTGCTGCTGC 2

RESULT 116
LOCUS AX753823 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 170 from Patent WO03037931.
ACCESSION AX753823
VERSION AX753823.1 GI:32166520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 Shannon, M. and Phan, T.
  TITLE Human angiotensin-like protein 1
  JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
  AMERSHAM Biosciences SV Corp. (US)
  LOCATION/Qualifiers
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Query Match
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 TGCTGTTGCTGCTGC 740
DB 15 TGCTGTTGCTGCTGC 1

RESULT 117
LOCUS AR102020 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 18 from patent US 6083731.
ACCESSION AR102020
VERSION AR102020.1 GI:12812818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Creteau, R., Bruce, J., Lupien, S., Lee, and Karp, F.
  TITLE Recombinant materials and methods for the production of limonene
  JOURNAL hydroxylases
  PATENT: US 6083731-A 18 04-JUL-2000;
  LOCATION/Qualifiers
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  source 1..19
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Best Local Similarity 84.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAA 1537
DB 19 DAAAAAAGTAAAA 1

RESULT 118
LOCUS AR134802 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6194185.
ACCESSION AR134802
VERSION AR134802.1 GI:14123707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Creteau, R., Bruce, J., Lupien, S., Lee, and Karp, F.
  TITLE Recombinant materials and methods for production of limonene
  JOURNAL hydroxylases
  PATENT: US 6194185-A 18 27-FEB-2001;
  LOCATION/Qualifiers
FEATURES
  source 1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  1.1%; Score 15; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAA 1537
DB 19 DAAAAAAGTAAAA 1

RESULT 119
LOCUS AR352460 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6589752.
ACCESSION AR352460
VERSION AR352460.1 GI:33757610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 19)
  Kong, Y., Chung, J.-Y., Bahk, Y.-Y., Kang, S.-Y. and Cho, S.-Y.
  TITLE Recombinant antigen of Taenia solium metacercodes
  JOURNAL Patent: US 6589752-A 6 08-JUL-2003;
  LOCATION/Qualifiers
FEATURES
  source 1..19
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
  1.1%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1241 CCTCATCTTGTGTTT 1255
DB 18 CCTCATCTTGTGTTT 4

RESULT 120
LOCUS E28098 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for analyzing DNA fragment.
ACCESSION E28098
VERSION E28098.1 GI:13018323
KEYWORDS
SOURCE JP 1999196874-A/9.
ORGANISM unidentified
REFERENCE
  1 (bases 1 to 20)
  Hideki, K. and Senshu, U.
  TITLE Method for analyzing DNA fragment
  JOURNAL Patent: JP 1999196874-A 9 27-JUL-1999;
  HITACHI LTD
  COMMENT OS Unidentified
  PN JP 1999196874-A/9
```

PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..20 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAGAAAAA 1537
DB 19 BAAAAA 1
RESULT 121
LOCUS AR294700/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6435 from patent US 6537751.
ACCESSION AR294700
VERSION AR294700.1 GI:31681984
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6435 25-MAR-2003;
FEATURES
source Location/Qualifiers
1..20 /organism='unknown'
/mol_type='genomic DNA'
Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 941 CCTCAGTCACCTTCT 955
DB 16 CCTCAGTCACCTTCT 2
RESULT 122
LOCUS AR307942 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 153 from patent US 6551826.
ACCESSION AR307942
VERSION AR307942.1 GI:31698698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watt, A.T.
TITLE Antisense modulation of raiid expression
JOURNAL Patent: US 6551826-A 153 22-APR-2003;
FEATURES
source Location/Qualifiers
1..20 /organism='unknown'
/mol_type='genomic DNA'

Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1539 GGAAGCAGATGTC 1553
DB 6 GGAAGCAGATGTC 20
RESULT 123
LOCUS AX048446/c 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 45 from Patent WO0071747.
ACCESSION AX048446
VERSION AX048446.1 GI:12225610
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Hoppe, H. U. and Burgeraller, P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 45 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source Location/Qualifiers
1..20 /organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Beschreibung der kunstlichen
Sequenz: Erkennungssystem'
Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1517 ATTAATAAAAAA 1531
DB 16 ATTAATAAAAAA 2
RESULT 124
LOCUS AX804844/c 21 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 1012 from Patent WO03060160.
ACCESSION AX804844
VERSION AX804844.1 GI:38521985
KEYWORDS
SOURCE Oreochromis niloticus (Nile tilapia)
ORGANISM Oreochromis niloticus
REFERENCE 1
AUTHORS Lie, Y., Slettan, A., Hoeyum, M. and Lingaas, F.
TITLE Verification of food origin based on nucleic acid pattern
recognition
JOURNAL Patent: WO 03060160-A 1012 24-JUN-2003;
Genomar ASA (NO)
FEATURES
source Location/Qualifiers
1..21 /organism='Oreochromis niloticus'
/mol_type='unassigned DNA'
/db_xref='taxon:8128'
Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 735 TGCTGCTTGTGAC 749
|||||

Db 19 TGCTGCTTGTGTGAC 5

RESULT 125
AR034896/c
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 126
AR034899
LOCUS AR034899 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 127
AR058305
LOCUS AR058305 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.

TITLE Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 128
AR097579/c
LOCUS AR097579 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 129
AR101834
LOCUS AR101834 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 25 from patent US 6083713.
ACCESSION AR101834
VERSION AR101834.1 GI:12812632
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manly,S.P., Kozlowski,M.R. and Neve,R.L.
TITLE Cloning and expression of betaAPP-C100 receptor (C100-R)
JOURNAL Patent: US 6083713-A 25 04-JUL-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAGAACAAAA 18

RESULT 130
ARI06506 18 bp DNA linear PAT 14-FEB-2001
LOCUS ARI06506
DEFINITION Sequence 30 from patent US 6107060.
ACCESSION ARI06506
VERSION ARI06506.1 GI:12821036
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
|||
1 AAAAAAAAAAAAAAAAAA 18

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 131
ARI06909/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS ARI06909
DEFINITION Sequence 70 from patent US 6107092.
ACCESSION ARI06909
VERSION ARI06909.1 GI:12821439
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1489 ATACATTAAATGCAGAAA 1506
|||
18 AAGATTAAATGCAGAAA 1

Db 18 AAGATTAAATGCAGAAA 1

RESULT 132
BD22596 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD22596/c
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
ACCESSION BD22596
VERSION BD22596.1 GI:33032366
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="unidentified"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
|||
1 AAAAAAAAAAAAAAAAAA 18

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 134
E28536/c

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
PF 09-AUG-1999 JP 2000563675
PR 07-AUG-1998 US 09/130973
PI MUTHIAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
PI KAMASAKI
PC C07H19/167, C07H19/067, C07H19/10, C07H19/20, C07H21/02, C12N15/00,
CC C12N15/00
CC Description of Artificial Sequence: antisense sequence FH
Key
FT source 1. .18
/organism="Artificial Sequence".
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
|||
1 AAAAAAAAAAAAAAAAAA 18

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 133
E28535 18 bp DNA linear PAT 18-JUN-2001
LOCUS E28535
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28535
VERSION E28535.1 GI:13025387
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 1999075880-A/2
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI, HIROSHI YOSHITAKURA, MASAHIDE NOZAKI PC
CC C12N15/09, C12Q1/68, G01N33/58, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1. .18
/organism="Unidentified".
Location/Qualifiers
1. .18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
|||
1 AAAAAAAAAAAAAAAAAA 18

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 134
E28536/c

LOCUS E28536 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28536
VERSION E28536.1 GI:13025388
KEYWORDS JP 1999075880-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 1999075880-A/3 23-MAR-1999;
CHEMO SERO THERAPEUT RES INST
COMMENT OS Unidentified
PN JP 1999075880-A/3
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
Topology: Linear;
FH Key Location/Qualifiers
FT source 1..18
Location/Qualifiers
1..18 /organism='Unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 135
LOCUS I79509 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION I79509
VERSION I79509.1 GI:3207799
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES Location/Qualifiers
1..18
source /organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 136
LOCUS ARI96702/c 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1167 from patent US 6350934.
ACCESSION ARI96702

VERSION ARI96702.1 GI:20246139
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P,Ann Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1167 26-FEB-2002;
FEATURES Location/Qualifiers
1..18
source /organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GCTGCGGCGCGCGGACG 447
|||||
18 GCTGCGGCGCGCGGCGG 1

RESULT 137
LOCUS ARI96704/c 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1169 from patent US 6350934.
ACCESSION ARI96704
VERSION ARI96704.1 GI:20246141
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P,Ann Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1169 26-FEB-2002;
FEATURES Location/Qualifiers
1..18
source /organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 GCGGCTCGGCGCGCGG 444
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18 GCTGCTGCGGCGGCGGCG 1

RESULT 138
LOCUS ARI215435/c 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION ARI215435
VERSION ARI215435.1 GI:23313691
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Iln,C.-I.P., Wallace,R.B., Cosman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES Location/Qualifiers
1..18
source /organism='unknown'
/mol_type='genomic DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 139
AR222464 18 bp DNA linear PAT 26-SEP-2002
LOCUS AR222464
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methode
JOURNAL Patent: US 6429300-A 24 06-AUG-2002;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 140
AR412363 18 bp DNA linear PAT 18-DEC-2003
LOCUS AR412363
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleosidic compounds and oligomeric compounds prepared therefrom
JOURNAL Patent: US 6639062-A 14 28-OCT-2003;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 141
AR473365 18 bp DNA linear PAT 20-FEB-2004
LOCUS AR473365
DEFINITION Sequence 9 from patent US 6686460.
ACCESSION AR473365
VERSION AR473365.1 GI:42708816

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Lin,C.-I.P., Wallace,R.B., Coesman,T. and French,C.
METHOD Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6686460-A 9 03-FEB-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 142
AR487019 18 bp DNA linear PAT 14-MAY-2004
LOCUS AR487019
DEFINITION Sequence 6 from patent US 6706476.
ACCESSION AR487019
VERSION AR487019.1 GI:47251966
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 6 16-MAR-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 143
AR487020 18 bp DNA linear PAT 14-MAY-2004
LOCUS AR487020
DEFINITION Sequence 7 from patent US 6706476.
ACCESSION AR487020
VERSION AR487020.1 GI:47251967
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 7 16-MAR-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 144

AX004875/c

LOCUS AX004875 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent WO910527.
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bayer,E. and Schwilz,J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
PATENT: WO 910527-A 4 04-MAR-1999;
SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
LOCATION/Qualifiers

1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl oligonucleotide"

FEATURES

source

1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 145
AX004879/c 18 bp RNA linear PAT 24-AUG-2000
LOCUS AX004879
DEFINITION Sequence 8 from Patent WO910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Bayer,E. and Schwilz,J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
PATENT: WO 910527-A 8 04-MAR-1999;
SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
LOCATION/Qualifiers

FEATURES

source

1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="2' methyl-modified oligonucleotide"
/mod_base=am

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 146
AX008117 18 bp DNA linear PAT 06-SEP-2000
LOCUS AX008117
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabino furanose and its analogues
PATENT: WO 9967378-A 2 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
LOCATION/Qualifiers

1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

FEATURES

source

1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 147
AX008118 18 bp RNA linear PAT 06-SEP-2000
LOCUS AX008118
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743.
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabino furanose and its analogues
PATENT: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
LOCATION/Qualifiers

FEATURES

source

1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 148

AX008122/c
LOCUS AX008122 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinoofuranose and its analogues
JOURNAL Patent: WO 967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES
source 1..18
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 149
AX008123 18 bp DNA linear PAT 06-SEP-2000
LOCUS AX008123
DEFINITION Sequence 8 from Patent WO967378.
ACCESSION AX008123
VERSION AX008123.1 GI:9995748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinoofuranose and its analogues
JOURNAL Patent: WO 967378-A 8 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 150
AX028843 18 bp DNA linear PAT 24-NOV-2000
LOCUS AX028843/c
DEFINITION Sequence 27 from Patent WO9733023.

ACCESSION AX028843
VERSION AX028843.1 GI:10189946
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Bruggiera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
FLORIGEME LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 151
AX047271 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047271
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M., Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 152
AX047273 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047273/c
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1

AUTHORS Mehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M.,
Gumbowski, K., and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 153
LOCUS AX104721/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 154
LOCUS AX104747/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 155
LOCUS AX105651/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stanton, L.W. and Kapoun, A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES Location/Qualifiers
SOURCE 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 156
LOCUS AX108642/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stanton, L.W. and Kapoun, A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES Location/Qualifiers
SOURCE 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 157
AX268883/c 18 bp DNA linear PAT 29-OCT-2001
LOCUS Sequence 84 from Patent WO0174901.
DEFINITION AX268883
ACCESSION AX268883
VERSION GI:16541910
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Scios Inc. (US)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligos corresponding to polylinker sequence."
FEATURES
source
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 158
AX355809/c 18 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 837 from Patent WO0197843.
DEFINITION AX355809
ACCESSION AX355809
VERSION GI:18620477
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Weiner, G. and Hartmann, G.
Method for enhancing antibody-induced cell lysis and treating
Cancer
Patent: WO 0197843-A 837 27-DEC-2001.
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"
FEATURES
source
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 159
AX547774/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 913 from Patent WO02053141.
DEFINITION AX547774
ACCESSION AX547774
VERSION GI:25812918
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct

artificial sequences.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
FEATURES
source
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 160
AX547800/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 939 from Patent WO02053141.
DEFINITION AX547800
ACCESSION AX547800
VERSION GI:25812944
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
FEATURES
source
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 161
AX814716/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS Sequence 1 from Patent WO03064441.
DEFINITION AX814716
ACCESSION AX814716
VERSION GI:39103916
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
Damha, M.J. and Parniak, M.A.
Oligonucleotides comprising alternating segments and uses thereof
Patent: WO 03064441-A 1 07-AUG-2003;
MCGILL UNIVERSITY (CA)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
FEATURES
source

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/note="Oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 162
AX814723/c AX814723 18 bp DNA linear PAT 05-DEC-2003
LOCUS Sequence 8 from Patent WO03064441.
AX814723
ACCESSION AX814723
VERSION AX814723.1 GI:39103922
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 8 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
misc_feature 1. .17
/note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 163
AX814724/c AX814724 18 bp DNA linear PAT 05-DEC-2003
LOCUS Sequence 9 from Patent WO03064441.
AX814724
ACCESSION AX814724
VERSION AX814724.1 GI:39103923
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 9 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
misc_feature 1. .15
/note="Residues 1-3, 7-9, and 13-15 are
2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 164
AX814725/c AX814725 18 bp DNA linear PAT 05-DEC-2003
LOCUS Sequence 10 from Patent WO03064441.
AX814725
ACCESSION AX814725
VERSION AX814725.1 GI:39103924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 10 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
misc_feature 1. .18
/note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 165
AX814736/c AX814736 18 bp RNA linear PAT 05-DEC-2003
LOCUS Sequence 21 from Patent WO03064441.
AX814736
ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Target RNA oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 166
BD085545/c BD085545 18 bp RNA linear PAT 27-AUG-2002
LOCUS
```

DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimada, K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 2 04-DEC-2001;
UNITECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAOI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC

FEATURES
source FH Key Location/Qualifiers
FT 1.18 /organism="Homo sapiens (human)".
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 167
LOCUS A68209 19 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION A68209
VERSION A68209.1 GI:4759376
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood, S.P., Moser, H.E., Altmann, K. and Douglas, M.E.
TITLE INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GEIGY AG (CH)
FEATURES
source 1.19 Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 168
LOCUS AR048767 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5821354.

ACCESSION AR048767
VERSION AR048767.1 GI:5971110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ieclerc, G. and Martel, R.
TITLE Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL Patent: US 5821354-A 1 13-OCT-1998;
FEATURES
source 1.19 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 169
LOCUS AR111371 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION AR111371
VERSION AR111371.1 GI:12828219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Leeds, J.M. and Cummins, L.L.
TITLE Fluorescence based nuclease assay
JOURNAL Patent: US 6127124-A 1 03-OCT-2000;
FEATURES
source 1.19 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 170
LOCUS AR111946 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 20 from patent US 6127533.
ACCESSION AR111946
VERSION AR111946.1 GI:12828794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 20 03-OCT-2000;
FEATURES
source 1.19 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;

Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1520	AAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						
RESULT 171									
LOCUS	AR111947/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence 21 from patent US 6127533.								
ACCESSION	AR111947								
VERSION	AR111947.1		GI:12828795						
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 19)								
TITLE	Cook, P.Dan., Manoharan, M. and Kawasaki, A.Mamoru.								
JOURNAL	2'-O-aminooxy-modified oligonucleotides								
FEATURES	Patent: US 6127533-A 21 03-Oct-2000;								
source	Location/Qualifiers								
	1..19								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match		1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity		88.9%;	Pred. No. 1.9e+02;						
Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1520	AAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						
RESULT 172									
LOCUS	AR111948/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence 22 from patent US 6127533.								
ACCESSION	AR111948								
VERSION	AR111948.1		GI:12828796						
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 19)								
TITLE	Cook, P.Dan., Manoharan, M. and Kawasaki, A.Mamoru.								
JOURNAL	2'-O-aminooxy-modified oligonucleotides								
FEATURES	Patent: US 6127533-A 22 03-Oct-2000;								
source	Location/Qualifiers								
	1..19								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match		1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity		88.9%;	Pred. No. 1.9e+02;						
Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1520	AAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						
RESULT 173									
LOCUS	AR111949/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence 23 from patent US 6127533.								
ACCESSION	AR111949								
VERSION	AR111949.1		GI:12828797						
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								

[illegible]

RESULT 176
AR11952/c
LOCUS AR11952 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6127533.
ACCESSION AR11952
VERSION AR11952.1 GI:12828800
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 26 03-OCT-2000;
FEATURES
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 177
AR11953/c
LOCUS AR11953 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 27 from patent US 6127533.
ACCESSION AR11953
VERSION AR11953.1 GI:12828801
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 27 03-OCT-2000;
FEATURES
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 178
AR11957/c
LOCUS AR11957 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 31 from patent US 6127533.
ACCESSION AR11957
VERSION AR11957.1 GI:12828805
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 31 03-OCT-2000;
FEATURES
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 179
AR11959/c
LOCUS AR11959 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 33 from patent US 6127533.
ACCESSION AR11959
VERSION AR11959.1 GI:12828807
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 33 03-OCT-2000;
FEATURES
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 180
AR11960/c
LOCUS AR11960 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 34 from patent US 6127533.
ACCESSION AR11960
VERSION AR11960.1 GI:12828808
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 34 03-OCT-2000;
FEATURES
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 181
AR11970/c
LOCUS AR11970 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 44 from patent US 6127533.
ACCESSION AR11970

VERSION AR11970.1 GI:12828818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6172533-A 44 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 182
AR124843/c
LOCUS AR124843 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6172209.
ACCESSION AR124843
VERSION AR124843.1 GI:14110204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 183
AR124844/c
LOCUS AR124844 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172209.
ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 184
AR124845/c
LOCUS AR124845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION AR124845
VERSION AR124845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 185
AR124846/c
LOCUS AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 186
AR124847/c
LOCUS AR124847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6172209.
ACCESSION AR124847
VERSION AR124847.1 GI:14110208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)

AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 24 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 187
AR124848/c AR124848 19 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 25 from patent US 6172209.
ACCESSION AR124848
VERSION AR124848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 188
AR124849/c AR124849 19 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 26 from patent US 6172209.
ACCESSION AR124849
VERSION AR124849.1 GI:14110210
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 26 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 189
AR124850/c AR124850 19 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 27 from patent US 6172209.
ACCESSION AR124850
VERSION AR124850.1 GI:14110211
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 27 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 190
AR124854/c AR124854 19 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 31 from patent US 6172209.
ACCESSION AR124854
VERSION AR124854.1 GI:14110215
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 31 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 191
AR124856/c AR124856 19 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 33 from patent US 6172209.
ACCESSION AR124856
VERSION AR124856.1 GI:14110217
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 33 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"

```

/mot_type="unassigned DNA"
Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAAGTAAA 1537
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 192
AR124857/c      19 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR124857
DEFINITION      Sequence 34 from patent US 6172209.
ACCESSION      AR124857
VERSION      AR124857.1 GI:14110218
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE      Aminoxy-modified oligonucleotides and methods for making same
JOURNAL      Patent: US 6172209-A 34 09-JAN-2001;
FEATURES
      Location/Qualifiers
      1..19
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAAGTAAA 1537
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 193
AR124867/c      19 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR124867
DEFINITION      Sequence 44 from patent US 6172209.
ACCESSION      AR124867
VERSION      AR124867.1 GI:14110228
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE      Aminoxy-modified oligonucleotides and methods for making same
JOURNAL      Patent: US 6172209-A 44 09-JAN-2001;
FEATURES
      Location/Qualifiers
      1..19
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAAGTAAA 1537
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 194
AR135291/c      19 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR135291
DEFINITION      Sequence 20 from patent US 6194598.
ACCESSION      AR135291
VERSION      AR135291.1 GI:14124196
```

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KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE      Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL      Patent: US 6194598-A 20 27-FEB-2001;
FEATURES
      Location/Qualifiers
      1..19
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAAGTAAA 1537
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 195
AR135292/c      19 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR135292
DEFINITION      Sequence 21 from patent US 6194598.
ACCESSION      AR135292
VERSION      AR135292.1 GI:14124197
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE      Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL      Patent: US 6194598-A 21 27-FEB-2001;
FEATURES
      Location/Qualifiers
      1..19
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAAGTAAA 1537
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 196
AR135293/c      19 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR135293
DEFINITION      Sequence 22 from patent US 6194598.
ACCESSION      AR135293
VERSION      AR135293.1 GI:14124198
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE      Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL      Patent: US 6194598-A 22 27-FEB-2001;
FEATURES
      Location/Qualifiers
      1..19
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 197
LOCUS AR135294 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6194598.
ACCESSION AR135294
VERSION AR135294.1 GI:14124199
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 23 27-FEB-2001;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 198
LOCUS AR135295 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6194598.
ACCESSION AR135295
VERSION AR135295.1 GI:14124200
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 24 27-FEB-2001;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 199
LOCUS AR135296 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION AR135296
VERSION AR135296.1 GI:14124201
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.

TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 25 27-FEB-2001;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 200
LOCUS AR135297 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6194598.
ACCESSION AR135297
VERSION AR135297.1 GI:14124202
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 26 27-FEB-2001;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 201
LOCUS AR135298 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 27 from patent US 6194598.
ACCESSION AR135298
VERSION AR135298.1 GI:14124203
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 27 27-FEB-2001;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
| | | | |
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 202

AR135302/c
LOCUS AR135302 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6194598.
ACCESSION AR135302
VERSION AR135302.1 GI:14124207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 31 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 203
AR135304/c
LOCUS AR135304 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6194598.
ACCESSION AR135304
VERSION AR135304.1 GI:14124209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 33 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 204
AR135305/c
LOCUS AR135305 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 34 from patent US 6194598.
ACCESSION AR135305
VERSION AR135305.1 GI:14124210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 34 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 205
AR135315/c
LOCUS AR135315 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 44 from patent US 6194598.
ACCESSION AR135315
VERSION AR135315.1 GI:14124220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 44 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 206
AR141898/c
LOCUS AR141898 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6147200.
ACCESSION AR141898
VERSION AR141898.1 GI:15101414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M., Kawasaki, A. M., Cook, P. Dan., Fraser, A. S. and Prakash, T. P.
TITLE 2'-O-acetamido modified monomers and oligomers
JOURNAL Patent: US 6147200-A 4 14-NOV-2000;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 207
AR153863/c
LOCUS AR153863 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6238624.
ACCESSION AR153863
VERSION AR153863.1 GI:15121916

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Unknown.
Unclassified.
1 (bases 1 to 19)
Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
Methods for transport in molecular biological analysis and
diagnostics
Patent: US 6238624-A 16-29-MAY-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 208
AR164173/c 19 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

AR164173
Sequence 6 from patent US 6271358.
AR164173
AR164173.1 GI:16235162
Unknown.
Unclassified.
1 (bases 1 to 19)
Manoharan,M., Mohan,V. and Boswell,H.
RNA targeted 2'-modified oligonucleotides that are conformationally
preorganized
Patent: US 6271358-A 6-07-AUG-2001;
Location/Qualifiers
1..19
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/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 209
BD196900/c 19 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD196900
Prostatic cancer gene.
BD196900
BD196900.1 GI:33006670
JP 2002516657-A/489.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 19)
Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
Prostatic cancer gene
Patent: JP 2002516657-A 489 11-JUN-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI

DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N1/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
PC C12N5/00,C12N5/00
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 4-4-187, mis2 FH Key
Location/Qualifiers
FT primer bind 1..19.
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1132 ATAGATGTTAAATTTT 1149
DB 2 ATAGATGTTAAATTTCT 19

RESULT 211
BD274438/c 19 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION

BD274438
Oligonucleotides having A-DNA form and B-DNA form conformational

ACCESSION BD274438.1 GI:33084206
VERSION BD274438.1
KEYWORDS JP 2002543215-A/15.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL Patent: JP 2002543215-A 15 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS JP 2002543215-A/15
PN JP 2002543215-A/15
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
FH Key Location/Qualifiers
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FT misc_feature (17) . (18)
FT misc_feature (18) . (19).
FEATURES Location/Qualifiers
source 1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 212
BD274439/c
LOCUS BD274439 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry.
ACCESSION BD274439.1 GI:33084207
VERSION BD274439.1
KEYWORDS JP 2002543215-A/16.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL Patent: JP 2002543215-A 16 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS JP 2002543215-A/16
PN JP 2002543215-A/16
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage

PH Key Location/Qualifiers
FT misc_feature (16) . (17)
FT misc_feature (17) . (18)
FT misc_feature (18) . (19).
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 213
BD274440/c
LOCUS BD274440 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry.
ACCESSION BD274440.1 GI:33084208
VERSION BD274440.1
KEYWORDS JP 2002543215-A/17.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL Patent: JP 2002543215-A 17 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS JP 2002543215-A/17
PN JP 2002543215-A/17
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC sub O linkage
CC 3' - O-MOE linkage; sub O linkage
CC 3' - O-MOE linkage; sub O linkage
CC 3' - O-MOE linkage; sub O linkage
FH Key Location/Qualifiers
FT misc_feature (15) . (16)
FT misc_feature (16) . (17)
FT misc_feature (17) . (18)
FT misc_feature (18) . (19)
FT misc_feature (19) . (19).
FEATURES Location/Qualifiers
source 1. .19
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 214
BD274441/c

LOCUS	BD274441	19 bp	DNA	linear	PAT 17-Jul-2003			
DEFINITION	Oligonucleotides having A-DNA form and B-DNA form confirmational geometry.							
ACCESSION	BD274441							
VERSION	BD274441.1	GI:33084209						
KEYWORDS	JP 2002543215-A/18.							
SOURCE	synthetic construct							
ORGANISM	synthetic construct							
REFERENCE	artificial sequences.							
AUTHORS	1 (bases 1 to 19)							
TITLE	Manoharan, M. and Mohan, V.							
	Oligonucleotides having A-DNA form and B-DNA form confirmational geometry							
JOURNAL	Patent: JP 2002543215-A 18 17-DEC-2002;							
COMMENT	ISIS PHARMACEUTICALS INC							
	OS Artificial Sequence							
	PN JP 2002543215-A/18							
	PD 17-DEC-2002							
	PF 03-MAY-2000 JP 2000615638							
	PR 03-MAY-1999 US 09/303586							
	PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN							
	PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,							
	PC C12N15/00							
	CC Oligonucleotide							
	CC sub O linkage							
	CC 2'-O-MOE; sub O linkage							
	CC 2'-O-MOE; sub O linkage							
	CC 2'-O-MOE; sub O linkage							
	FH Key							
	FT misc_feature Location/Qualifiers							
	FT misc_feature (15)..(16)							
	FT misc_feature (16)..(17)							
	FT misc_feature (17)..(18)							
	FT misc_feature (18)..(19)							
	FT misc_feature (19)..(19).							
FEATURES	Location/Qualifiers							
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	/mol_type="genomic DNA"							
	/db_xref="taxon:32630"							
Query Match	1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity	88.9%;	Pred. No. 1.9e+02;						
Matches 16;	Conservative 0;	Indels 2;	Gaps 0;					
Oy	1520 AAAAAAAAAAGTAAA	1537						
Db	19 AAAAAAAAAAAAAAAAAA	2						
RESULT 215								
LOCUS	BD274449/c	19 bp	DNA	linear	PAT 17-Jul-2003			
DEFINITION	Oligonucleotides having A-DNA form and B-DNA form confirmational geometry.							
ACCESSION	BD274449							
VERSION	BD274449.1	GI:33084217						
KEYWORDS	JP 2002543215-A/26.							
SOURCE	synthetic construct							
ORGANISM	synthetic construct							
	artificial sequences.							
	1 (bases 1 to 19)							
	Manoharan, M. and Mohan, V.							
	Oligonucleotides having A-DNA form and B-DNA form confirmational geometry							
JOURNAL	Patent: JP 2002543215-A 26 17-DEC-2002;							
COMMENT	ISIS PHARMACEUTICALS INC							
	OS Artificial Sequence							
	PN JP 2002543215-A/26							
	PD 17-DEC-2002							

PC	C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC	C12N15/00
CC	Oligonucleotide
CC	2'-modified T linkage
CC	2'-modified T linkage
CC	2'-modified T linkage
CC	2'-modified T linkage
PH	Key
FT	misc.feature (16), (17)
FT	misc.feature (17), (18)
FT	misc.feature (18), (19)
FT	misc.feature (19), (19)
FEATURES	Location/Qualifiers
source	1..19
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
Query Match	1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity	88.9%; Pred. No. 1.9e+02;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	1520 AAAAAAAAAAGTAAAA 1537
Db	19 AAAAAAAAAAAAAAAAAA 2
RESULT 216	
LOCUS	AR205798 19 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 15 from patent US 6369209.
ACCESSION	AR205798
VERSION	AR205798.1 GI:21503472
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 19)
AUTHORS	Manoharan,M. and Mohan,V.
TITLE	Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL	Patent: US 6369209-A 15 09-APR-2002;
FEATURES	Location/Qualifiers
source	1..19
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity	88.9%; Pred. No. 1.9e+02;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	1520 AAAAAAAAAAGTAAAA 1537
Db	19 AAAAAAAAAAAAAAAAAA 2
RESULT 217	
LOCUS	AR205799 19 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 16 from patent US 6369209.
ACCESSION	AR205799
VERSION	AR205799.1 GI:21503473
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 19)
AUTHORS	Manoharan,M. and Mohan,V.
TITLE	Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL	Patent: US 6369209-A 16 09-APR-2002;
FEATURES	Location/Qualifiers
source	1..19

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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 218
LOCUS AR205800 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6369209.
ACCESSION AR205800
VERSION AR205800.1 GI:21503474
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL Patent: US 6369209-A 17 09-APR-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 219
LOCUS AR205801 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6369209.
ACCESSION AR205801
VERSION AR205801.1 GI:21503476
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL Patent: US 6369209-A 18 09-APR-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 220
LOCUS AR205809 19 bp DNA linear PAT 20-JUN-2002
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DEFINITION Sequence 26 from patent US 6369209.
ACCESSION AR205809
VERSION AR205809.1 GI:21503486
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL Patent: US 6369209-A 26 09-APR-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 221
LOCUS AR213490 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403779.
ACCESSION AR213490
VERSION AR213490.1 GI:23310721
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Kawaaski,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 1 11-JUN-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 222
LOCUS AR213491 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 2 from patent US 6403779.
ACCESSION AR213491
VERSION AR213491.1 GI:23310722
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Kawaaski,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 2 11-JUN-2002;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
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/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 223
AR213492/c AR213492 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213492/c
DEFINITION Sequence 3 from patent US 6403779.
ACCESSION AR213492
VERSION AR213492.1 GI:23310723
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 3 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 224
AR213493/c AR213493 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213493/c
DEFINITION Sequence 4 from patent US 6403779.
ACCESSION AR213493
VERSION AR213493.1 GI:23310724
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 225
AR213494/c AR213494 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213494/c
DEFINITION Sequence 5 from patent US 6403779.

ACCESSION AR213494
VERSION AR213494.1 GI:23310725
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 226
AR213495/c AR213495 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213495/c
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 6 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 227
AR213496/c AR213496 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213496/c
DEFINITION Sequence 7 from patent US 6403779.
ACCESSION AR213496
VERSION AR213496.1 GI:23310727
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 228
AR213497/c AR213497 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 229
AR213501/c AR213501 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6403779.
ACCESSION AR213501
VERSION AR213501.1 GI:23310732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 12 11-JUN-2002;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 230
AR213502/c AR213502 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 14 from patent US 6403779.
ACCESSION AR213502

VERSION AR213502.1 GI:23310733
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 14 11-JUN-2002;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 231
AR213503/c AR213503 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 15 from patent US 6403779.
ACCESSION AR213503
VERSION AR213503.1 GI:23310734
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 15 11-JUN-2002;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 232
AR213512/c AR213512 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6403779.
ACCESSION AR213512
VERSION AR213512.1 GI:23310743
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 233
AR222465 19 bp DNA linear PAT 26-SEP-2002
LOCUS AR222465
DEFINITION Sequence 25 from patent US 6429300.
ACCESSION AR222465
VERSION AR222465.1 GI:2332996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 25 06-AUG-2002;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

RESULT 234
AR237463 19 bp DNA linear PAT 20-DEC-2002
LOCUS AR237463
DEFINITION Sequence 1 from patent US 6465628.
ACCESSION AR237463
VERSION AR237463.1 GI:27282213
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and Guzaev,A.
TITLE Process for the synthesis of oligomeric compounds
JOURNAL Patent: US 6465628-A 1 15-OCT-2002;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 235
AR295557 19 bp DNA linear PAT 12-JUN-2003
LOCUS AR295557
DEFINITION Sequence 7292 from patent US 6537751.
ACCESSION AR295557
VERSION AR295557.1 GI:31682841
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7292 25-MAR-2003;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1103 TCTACTTCATTTTCC 1120
Db 18 TCTCATTTCCATTTTCC 1

RESULT 236
AR321589 19 bp DNA linear PAT 17-AUG-2003
LOCUS AR321589
DEFINITION Sequence 10 from patent US 6562960.
ACCESSION AR321589
VERSION AR321589.1 GI:33706818
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
TITLE Oligonucleotide analogues
JOURNAL Patent: US 6562960-A 10 13-MAY-2003;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 237
AR359804 19 bp DNA linear PAT 17-AUG-2003
LOCUS AR359804
DEFINITION Sequence 3 from patent US 6593466.
ACCESSION AR359804
VERSION AR359804.1 GI:33766602
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guanine-rich functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 3 15-JUN-2003;
FEATURES Location/Qualifiers
1..19
source /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 238
LOCUS AR359805 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6593466.
ACCESSION AR359805
VERSION AR359805.1 GI:33766603
KEYWORDS
SOURCE
ORGANISM
Unklassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Granidinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 4 15-JUL-2003;
FEATURES
LOCATION/Qualifiers
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 239
LOCUS AR359806/c 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6593466.
ACCESSION AR359806
VERSION AR359806.1 GI:33766604
KEYWORDS
SOURCE
ORGANISM
Unklassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Granidinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 5 15-JUL-2003;
FEATURES
LOCATION/Qualifiers
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 240
LOCUS AR367447/c 19 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6329519.
ACCESSION AR367447
VERSION AR367447.1 GI:34600659
KEYWORDS
SOURCE
ORGANISM
Unklassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.

TITLE Intermediates for oligonucleotide synthesis
JOURNAL Patent: US 6329519-A 4 11-DEC-2001;
FEATURES
LOCATION/Qualifiers
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 241
LOCUS AR399177/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE
ORGANISM
Unklassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES
LOCATION/Qualifiers
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 242
LOCUS AR399178 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE
ORGANISM
Unklassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES
LOCATION/Qualifiers
1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 243

AR403601/c
LOCUS AR403601 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6624294.
ACCESSION AR403601
VERSION AR403601.1 GI:40151187
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 1 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 244
AR403602/c
LOCUS AR403602 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6624294.
ACCESSION AR403602
VERSION AR403602.1 GI:40151188
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 2 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 245
AR403603/c
LOCUS AR403603 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6624294.
ACCESSION AR403603
VERSION AR403603.1 GI:40151189
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES
Source Location/Qualifiers

source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 246
AR403604/c
LOCUS AR403604 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 247
AR403605/c
LOCUS AR403605 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION AR403605
VERSION AR403605.1 GI:40151191
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 5 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 248
AR403606/c

LOCUS AR403606 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6624294.
ACCESSION AR403606
VERSION AR403606.1 GI:40151192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 6 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 249
LOCUS AR403607/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6624294.
ACCESSION AR403607
VERSION AR403607.1 GI:40151193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 7 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 250
LOCUS AR403608/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6624294.
ACCESSION AR403608
VERSION AR403608.1 GI:40151194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 8 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19

/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 251
LOCUS AR403612/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6624294.
ACCESSION AR403612
VERSION AR403612.1 GI:40151198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 12 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 252
LOCUS AR403613/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6624294.
ACCESSION AR403613
VERSION AR403613.1 GI:40151199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 14 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 253
LOCUS AR403614/c 19 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 254
AR403623/C
LOCUS AR403623 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6624294.
ACCESSION AR403623
VERSION AR403623.1 GI:40151209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 25 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 255
AR412338/C
LOCUS AR412338 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.D., Manoharan,M., Maier,M. and An,H.
TITLE C3'-methylene hydrogen phosphate oligomers and related compounds
JOURNAL Patent: US 6639061-A 1 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 256
AR432616/C
LOCUS AR432616 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6653458.
ACCESSION AR432616
VERSION AR432616.1 GI:40195149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinosso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 6 25-NOV-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 257
AR432617/C
LOCUS AR432617 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653458.
ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinosso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 258
AR451262/C
LOCUS AR451262 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5 from patent US 6673912.
ACCESSION AR451262
VERSION AR451262.1 GI:42682240
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Cook,P.D.
TITLE 2'-O-aminomethyloxymethyl-modified oligonucleotides
JOURNAL Patent: US 6673912-A 5 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 259
LOCUS AR451282 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 26 from patent US 6673912.
ACCESSION AR451282
VERSION AR451282.1 GI:42682260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Cook,P.D.
TITLE 2'-O-aminomethyloxymethyl-modified oligonucleotides
JOURNAL Patent: US 6673912-A 26 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 260
LOCUS AX059378 19 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 111 from Patent WO0055325.
ACCESSION AX059378
VERSION AX059378.1 GI:12311483
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL rosidae; euroside II; Brassicales; Brassicaceae; Arabidopsi.
FEATURES Location/Qualifiers
source 1..19
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

Query Match 1.1%; Score 14.8; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1535 AAAGGAGGACGAGATGT 1552
Db 18 AATGGAGAGGCGGATGT 1

RESULT 261
LOCUS AX132398 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3616 from Patent WO0130362.
ACCESSION AX132398
VERSION AX132398.1 GI:14138703
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Robbings,J.M. and Tritz,R.
FEATURES Ribozyme therapy for the treatment of proliferative skin and eye
source diseases
IMMUSOL, INC. (US)
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1305 ATTTTCTTATTTCAGA 1322
Db 18 ATTTCTTTATTTCAGA 1

RESULT 262
LOCUS AX226133 19 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 52 from Patent WO0160856.
ACCESSION AX226133
VERSION AX226133.1 GI:15555445
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS artificial sequences.
TITLE Vlkhuia,M.
JOURNAL vnglom gene and its mutations causing disorders with a vascular
component
Patent: WO 0160856-A 52 23-AUG-2001;
FEATURES LOCATION/QUALIFIERS
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 GCGACGCTCTGTTCTG 1000
Db 2 GCGACGCTCTGTCGTG 19

RESULT 263
AX349249/c 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 33 from Patent WO0202810.
ACCESSION AX349249
VERSION AX349249.1 GI:18615281
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ermentrout,E., Kaiser,T.,
Schulz,T. and Wagner,G.
TITLE Method for qualitative and/or quantitative detecting of molecular
interactions on probe arrays
JOURNAL Patent: WO 0202810-A 33 10-JAN-2002;
Clondias Chip Technologies GmbH (DE)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide sonde"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 264
BD087505/c 19 bp DNA linear PAT 27-AUG-2002
LOCUS BD087505
DEFINITION Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION BD087505
VERSION BD087505.1 GI:22633115
KEYWORDS JP 2001525193-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Sonowaki,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
NANOGEN INC
OS Artificial Sequence
PN JP 2001525193-A/16
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOMSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER, CARL F EDMAN
PC C1201/66; C12N15/09; C12N15/00
CC Description of Artificial Sequence: Amino
conjugate to provide
CC with dyes reactivity
FH key Location/Qualifiers
FT source 1..19
Location/Qualifiers
1..19 /organism='Artificial Sequence'.
FEATURES
source 1..19
Location/Qualifiers
1..19 /organism="synthetic construct"
/mol_type="genomic DNA"

/db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 265
AR030917/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR030917
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T., Albert., Cornish,E., Cecily., Kovacic,F., Tanaka,Y. and
Lester,D., Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 266
AR064875/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR064875
DEFINITION Sequence 5 from patent US 5849480.
ACCESSION AR064875
VERSION AR064875.1 GI:5995091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gros,P., Kurfurst,R., Battail,N. and Piga,N.
TITLE Process and device for assaying a hapten
JOURNAL Patent: US 5849480-A 5 15-DEC-1998;
FEATURES
source 1..20
Location/Qualifiers
1..20 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 267
AR080000 20 bp DNA linear PAT 31-AUG-2000
LOCUS AR080000
DEFINITION Sequence 83 from patent US 5968524.

ACCESSION AR080000
VERSION AR080000.1 GI:1006735
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Watson,J.D. and Tan,P.L.J.
METHODS Methods and compounds for the treatment of immunologically-mediated
JOURNAL Peoriasis
FEATURES Patent: US 5968524-A 83 19-OCT-1999;
source location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 86.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

RESULT 268
AR085926 20 bp DNA linear PAT 07-SEP-2000
LOCUS AR085926
DEFINITION Sequence 83 from patent US 5985287.
ACCESSION AR085926
VERSION AR085926.1 GI:10012692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Skinner,M. and Prestidge,R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
JOURNAL Infections
FEATURES Patent: US 5985287-A 83 16-NOV-1999;
source location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

RESULT 269
AR087520 20 bp DNA linear PAT 07-SEP-2000
LOCUS AR087520
DEFINITION Sequence 1 from patent US 5986084.
ACCESSION AR087520
VERSION AR087520.1 GI:10014263
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weise,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: US 5986084-A 1 16-NOV-1999;
FEATURES location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 20 AAAAAAAAAAAAAAAAA 3

RESULT 270
AR093312 20 bp DNA linear PAT 08-SEP-2000
LOCUS AR093312
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

RESULT 271
AR118970 20 bp DNA linear PAT 16-MAY-2001
LOCUS AR118970
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES location/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 20 AAAAAAAAAAAAAAAAA 3

RESULT 272
AR121540 20 bp DNA linear PAT 16-MAY-2001
LOCUS AR121540
DEFINITION Sequence 76 from patent US 6159734.
ACCESSION AR121540
VERSION AR121540.1 GI:14105116
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Borchers, A.H. and Baker, B.F.
TITLE Antisense modulation of peroxisome proliferator-activated receptor
gamma expression
JOURNAL Patent: US 6159734-A 76 12-DEC-2000;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 745 GTGACGGATCGCTTCT 762
Db 2 GTGAAGAAATCGCTTCT 19

RESULT 273
AR121692 20 bp DNA linear PAT 16-MAY-2001
LOCUS AR121692
DEFINITION Sequence 83 from patent US 6160093.
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 274
AR123335 20 bp DNA linear PAT 16-MAY-2001
LOCUS AR123335
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brice, T.C. and Dev, A.P.
TITLE Decylmethyl alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 275
AR139960 20 bp DNA linear PAT 16-JUN-2001
LOCUS AR139960/c
DEFINITION Sequence 32 from patent US 6207417.
ACCESSION AR139960
VERSION AR139960.1 GI:14482456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 32 27-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 276
AR139962 20 bp DNA linear PAT 16-JUN-2001
LOCUS AR139962/c
DEFINITION Sequence 34 from patent US 6207417.
ACCESSION AR139962
VERSION AR139962.1 GI:14482458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 34 27-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 277
AR140279 20 bp DNA linear PAT 16-JUN-2001
LOCUS AR140279/c
DEFINITION Sequence 32 from patent US 6207454.
ACCESSION AR140279
VERSION AR140279.1 GI:14482775
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.

TITLE Method for enhancing the efficiency of gene transfer with stem cell
JOURNAL factor (SCF) polypeptide
Patent: US 6207454-A 32 27-MAR-2001;
LOCATION/Qualifiers
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAGTAAAA 1

RESULT 278
ARI40281/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40281
DEFINITION Sequence 34 from patent US 6207454.
ACCESSION ARI40281
VERSION ARI40281.1 GI:14482777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell
JOURNAL factor (SCF) polypeptide
Patent: US 6207454-A 34 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAGTAAAA 1

RESULT 279
ARI40557/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40557
DEFINITION Sequence 32 from patent US 6207802.
ACCESSION ARI40557
VERSION ARI40557.1 GI:14483053
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 32 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAGTAAAA 1

RESULT 280
ARI40559/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40559
DEFINITION Sequence 34 from patent US 6207802.
ACCESSION ARI40559
VERSION ARI40559.1 GI:14483055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 34 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAGTAAAA 1

RESULT 281
ARI41070/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI41070
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION ARI41070
VERSION ARI41070.1 GI:14483566
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
JOURNAL backbone oligomeric compounds
Patent: US 6207819-A 1 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAGTAAAA 3

RESULT 282
ARI54115/c 20 bp DNA linear PAT 08-AUG-2001
LOCUS ARI54115
DEFINITION Sequence 14 from patent US 6238865.
ACCESSION ARI54115
VERSION ARI54115.1 GI:15122168
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Huang, Z. and Szostak, J.W.
TITLE Simple and efficient method to label and modify 3'-termini of RNA
using DNA polymerase and a synthetic template with defined overhang
nucleotides

JOURNAL Patent: US 623865-A 14 29-MAY-2001;
FEATURES
SOURCE
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 283
LOCUS AR164658 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 13 from patent US 6274321.
ACCESSION AR164658
VERSION AR164658.1 GI:16237754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Blumberg, B.
TITLE High throughput functional screening of cDNAs
JOURNAL Patent: US 6274321-A 13 14-AUG-2001;
FEATURES
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 284
LOCUS BD218101 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218101
VERSION BD218101.1 GI:33027871
KEYWORDS JP 2002514385-A/26.
SOURCE synthetic construct
ORGANISM artificial sequence.
1 (bases 1 to 20)
REFERENCE Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Preatid, R.L.
AUTHORS Compositions derived from mycobacterium vaccae and methods for their use.
JOURNAL Patent: JP 2002514385-A 26 21-MAY-2002;
COMMENT GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Artificial Sequence
PN JP 2002514385-A/26
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES MARSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,

PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC (C12N15/09, C12R1:32), C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Made in a lab
FH Key
FT source 1. .20
Location/Qualifiers
/organism="Artificial Sequence".
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 285
LOCUS BD234126 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION BD234126
VERSION BD234126.1 GI:33043896
KEYWORDS JP 2002532072-A/14.
SOURCE synthetic construct
ORGANISM artificial sequence.
1 (bases 1 to 20)
REFERENCE Lipovsek, D.
AUTHORS Protein skeleton of antibody mimetics and other binding proteins
JOURNAL Patent: JP 2002532072-A 14 02-OCT-2002;
COMMENT PHYLOS INC
OS Artificial Sequence
PN JP 2002532072-A/14
PD 02-OCT-2002
PF 09-DEC-1999 JP 2000587187
PR 10-DEC-1998 US 60/111737
PI DASA LIPOVSEK
PC C12N15/09, C07K14/04, C07K14/78, C07K16/46, C07K17/00, C07K19/00, PC
C12P21/02,
PC C12N15/00
CC Puromycin linker oligonucleotide
FH Key
FT source 1. .20
Location/Qualifiers
/organism="Artificial Sequence".
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 286
LOCUS CQ759610 20 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 40 from Patent WO2003106672.
ACCESSION CQ759610
VERSION CQ759610.1 GI:44849560
KEYWORDS
SOURCE synthetic construct

ORGANISM	synthetic construct artificial sequences.					
REFERENCE TITLE	1 Hayashizaki,Y., Carninci,P. and Harbers,M.T. Method of utilizing the 5' end of transcribed nucleic acid regions for cloning and analysis					
JOURNAL	Patent: WO 2003106672-A 40 24-DEC-2003; Riken (JP), Kabushiki Kaisha Dnaform (JP)					
FEATURES	Location/Qualifiers					
source	1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="lag8"					
Query Match	1.1%; Score 14.8; DB 1; Length 20;					
Best Local Similarity	88.9%; Pred.No. 1.8e+02;					
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Oy	545 TGTGGTCCGTCGTGCCTG 562 Db 2 TGTGTGTGTGTGTGCCTG 19					
RESULT 287						
E12676/c						
LOCUS	E12676 20 bp DNA linear PAT 27-APR-1999					
DEFINITION	Anti-HTLV-1 antisense oligonucleotide.					
ACCESSION	E12676					
VERSION	E12676.1 GI:3251508					
KEYWORDS	JP 1997052898-A/10.					
SOURCE	unidentified					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 20) Mazuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N. AUTHORS TITLE ANTI-HTLV-I ANTI-SENSE OLIGONUCLEOTIDE JOURNAL Patent: JP 1997052898-A 10 25-FEB-1997; SOYAKU GIUTSU KENKYUSHO:KK					
COMMENT	OS None OC Artificial sequences. PN JP 1997052898-A/10 PD 25-FEB-1997 PF 09-AUG-1995 JP 1995224606 PI MIZUDUCHI MASATSUGU, KUROSAKI NAKO, MAKINO KEISUKE, PI KOYANAGI YOSHIO, PC YAMAMOTO NAOKI PC C07H21/04//A61K31/70; CC strandedness: Single; CC topology: linear; CC hypothetical: No; CC anti-sense: Yes; FH Key FH Location/Qualifiers FT source 1..20 Location/Qualifiers 1..20 /organism='Artificial sequences'. location/Qualifiers 1..20 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"					
FEATURES						
source						
Query Match	1.1%; Score 14.8; DB 1; Length 20;					
Best Local Similarity	88.9%; Pred.No. 1.8e+02;					
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Oy	1520 AAAAAAAAAAAAGTAATA 1537 Db 20 AAAAAAAAAAAAAAAAAAAAA 3					
RESULT 288						
E128309/c						

LOCUS	128309	20 bp	DNA	linear	PAT 06-FEB-1997
DEFINITION	Sequence 20 from patent US 5569832.				
ACCESSION	128309				
VERSION	128309.1	GI:1819085			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.				
JOURNAL	Genetic sequences encoding flavonoid pathway enzymes and uses				
FEATURES	therefor				
source	Patent: US 5569832-A 20 29-OCT-1996;				
	Location/Qualifiers				
	1..20				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	1.1%; Score 14.8; DB 1;	Length 20;			
Best Local Similarity	88.9%;	Pred. No. 1.8e+02;			
Matches	16; Conservative	0; Mismatches	2; Indels	0; Gaps	0;
QY	1519 TAAAAAAAAGTAAA	1536			
Db	18 TAAAAAAAAGTAAA	1			
RESULT 289					
LOCUS	136180	20 bp	DNA	linear	PAT 13-MAY-1997
DEFINITION	Sequence 16 from patent US 5605662.				
ACCESSION	136180				
VERSION	136180.1	GI:2086693			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Heiler,M.J. and Tu,E.				
JOURNAL	Active programmable electronic devices for molecular biological				
FEATURES	analysis and diagnostics				
source	Patent: US 5605662-A 16 25-FEB-1997;				
	Location/Qualifiers				
	1..20				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	1.1%; Score 14.8; DB 1;	Length 20;			
Best Local Similarity	88.9%;	Pred. No. 1.8e+02;			
Matches	16; Conservative	0; Mismatches	2; Indels	0; Gaps	0;
QY	1520 AAAAAAAAAGTAAA	1537			
Db	20 AAAAAAAAAGTAAA	3			
RESULT 290					
LOCUS	147310	20 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 11 from patent US 5639870.				
ACCESSION	147310				
VERSION	147310.1	GI:2471275			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.				
JOURNAL	Genetic sequences encoding flavonoid pathway enzymes and uses				
FEATURES	therefor				
source	Patent: US 5639870-A 11 17-JUN-1997;				
	Location/Qualifiers				
	1..20				

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1519 TAAAAAAGTAAAG 1536
Db 18 TAAAAAAGTAAAG 1

RESULT 291
LOCUS AR213738 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 83 from patent US 6406704.
ACCESSION AR213738
VERSION AR213738.1 GI:23311025
KEYWORDS
SOURCE .
ORGANISM unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan, P., Viesser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 83 18-JUN-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 1 AAAAAAAGTAAAG 18

RESULT 292
LOCUS AR222466 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 26 from patent US 6429300.
ACCESSION AR222466
VERSION AR222466.1 GI:23239997
KEYWORDS
SOURCE .
ORGANISM unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 26 06-AUG-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 1 AAAAAAAGTAAAG 18

RESULT 293
LOCUS AR231312 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 49 from patent US 6451968.

ACCESSION AR231312
VERSION AR231312.1 GI:27272243
KEYWORDS
SOURCE .
ORGANISM unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Egholm, M., Nielsen, P., Buchardt, O., Dueholm, K.L., Christensen, L., Coull, J.M., Kieley, J. and Griffith, M.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6451968-A 49 17-SEP-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1521 AAAAAAAGTAAAG 1539
Db 19 AAAAAAAGTAAAG 1

RESULT 294
LOCUS AR236083 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6462184.
ACCESSION AR236083
VERSION AR236083.1 GI:27279782
KEYWORDS
SOURCE .
ORGANISM unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maiter, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 1 08-OCT-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 20 AAAAAAAGTAAAG 3

RESULT 295
LOCUS AR274394 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 55 from patent US 6506564.
ACCESSION AR274394
VERSION AR274394.1 GI:29706840
KEYWORDS
SOURCE .
ORGANISM unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storzoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: US 6506564-A 55 14-JAN-2003;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 296
AR343047/c AR343047 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 10 from patent US 6576752.
ACCESSION AR343047
VERSION AR343047.1 GI:33738375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M., Lomberg, H., Sato, H. and Vitra, P.
TITLE Aminooxy functionalized oligomers
JOURNAL Patent: US 6576752-A 10-10-JUN-2003;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 297
AR344936 AR344936 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 55 from patent US 6582921.
ACCESSION AR344936
VERSION AR344936.1 GI:33741017
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6582921-A 55-24-JUN-2003;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 298
AR365970 AR365970 20 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 83 from patent US 6328978.
DEFINITION

ACCESSION AR365970
VERSION AR365970.1 GI:34598223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson, J.D., Tan, P.L.J. and Prestidge, R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 83-11-DEC-2001;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 299
AR382312 AR382312 20 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 55 from patent US 6610491.
ACCESSION AR382312
VERSION AR382312.1 GI:40090724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6610491-A 55-26-AUG-2003;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 300
AR429653 AR429653 20 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 55 from patent US 6645721.
ACCESSION AR429653
VERSION AR429653.1 GI:40189949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6645721-A 55-11-NOV-2003;
FEATURES Location/Qualifiers
1..20

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

RESULT 301
AR447441
LOCUS      AR447441      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6673548.
ACCESSION AR447441
VERSION    AR447441.1 GI:42675765
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6673548-A 55 06-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

RESULT 302
AR451990
LOCUS      AR451990      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6677122.
ACCESSION AR451990
VERSION    AR451990.1 GI:42683297
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6677122-A 55 13-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

RESULT 303
AR451990
LOCUS      AR451990      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6677122.
ACCESSION AR451990
VERSION    AR451990.1 GI:42683297
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6677122-A 55 13-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"
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AR454776
LOCUS      AR454776      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6682895.
ACCESSION AR454776
VERSION    AR454776.1 GI:42688297
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6682895-A 55 27-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

RESULT 304
AR488890/c
LOCUS      AR488890/c      20 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 7 from patent US 6709818.
ACCESSION AR488890
VERSION    AR488890.1 GI:47255117
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.
TITLE      Methods of diagnosing and treating hepatic cell proliferative
            disorders
JOURNAL    Patent: US 6709818-A 7 23-MAR-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1518 TTAATAAAAAAAAAAGTAA 1535
      19 TTAATAAAAAAAAAAATTA 2

RESULT 305
AR489044
LOCUS      AR489044      20 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6709825..
ACCESSION AR489044
VERSION    AR489044.1 GI:47255475
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
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JOURNAL Patent: US 6709825-A 55 23-MAR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 306
AR494116 AR494116 20 bp DNA linear PAT 15-MAY-2004
LOCUS
DEFINITION Sequence 55 from patent US 6720147.
ACCESSION AR494116
VERSION AR494116.1 GI:47266895
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Minkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6720147-A 55 13-APR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 307
AR494728 AR494728 20 bp DNA linear PAT 15-MAY-2004
LOCUS
DEFINITION Sequence 55 from patent US 6720411.
ACCESSION AR494728
VERSION AR494728.1 GI:47269581
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Minkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6720411-A 55 13-APR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 308
AX004876 AX004876 20 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 5 from Patent WO9910527.
ACCESSION AX004876
VERSION AX004876.1 GI:9928276
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 5 04-MAR-1999;
SWEDEBUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="phosphorchiolate oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 309
AX045779 AX045779 20 bp DNA linear PAT 24-NOV-2000
LOCUS
DEFINITION Sequence 9 from Patent WO0067023.
ACCESSION AX045779
VERSION AX045779.1 GI:11344146
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 9 09-NOV-2000;
CRG Immunopharmaceuticals GmbH (DE); UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
misc_feature 1
/note="modified with digoxigenin"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 310
AX045787 AX045787 20 bp DNA linear PAT 24-NOV-2000
LOCUS
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787

VERSION AX045787.1 GI:11344154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
1..20
/note="phosphorothioate backbone"
misc_feature
1
/note="modified with digoxigenin"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 311
AX045790/c
LOCUS AX045790 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 20 from Patent WO0067023.
ACCESSION AX045790
VERSION AX045790.1 GI:11344157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 312
AX056597/c
LOCUS AX056597 20 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 241 from Patent WO0073469.
ACCESSION AX056597
VERSION AX056597.1 GI:12229186
KEYWORDS
SOURCE Murinae gen. sp.
ORGANISM Murinae gen. sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE 1
AUTHORS Ploewman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
TITLE Protein Kinases
JOURNAL Patent: WO 0073469-A 241 07-DEC-2000;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
1..20
/organism="Murinae gen. sp."
/mol_type="unassigned DNA"
/db_xref="taxon:39108"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 698 CTGCTGAATGAGTCGCG 715
Db 20 CTGCTCAATGCTGTCGCG 3
RESULT 313
AX104034/c
LOCUS AX104034 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 226 from Patent WO0122972.
ACCESSION AX104034
VERSION AX104034.1 GI:13920231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 314
AX104364/c
LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
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Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 315
LOCUS AX104368 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 560 from Patent WO0122972.
ACCESSION AX104368
VERSION AX104368.1 GI:13920565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kriegl, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 560 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 316
LOCUS AX196224 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 55 from Patent WO0151665.
ACCESSION AX196224
VERSION AX196224.1 GI:15386427
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
TITLE Elghanian, R., Taton, T.A. and Li, Z.
JOURNAL Nanoparticles having oligonucleotides attached thereto and uses
therefor
Patent: WO 0151665-A 55 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 317
LOCUS AX196239 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 70 from Patent WO0151665.
ACCESSION AX196239
VERSION AX196239.1 GI:15386442
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
TITLE Elghanian, R., Taton, T.A. and Li, Z.
JOURNAL Nanoparticles having oligonucleotides attached thereto and uses
therefor
Patent: WO 0151665-A 70 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 318
LOCUS AX354974 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent WO0197843.
ACCESSION AX354974
VERSION AX354974.1 GI:18619641
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 2 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 319
LOCUS AX355810/c 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 838 from Patent WO0197843.
ACCESSION AX355810
VERSION AX355810.1 GI:18620478
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and creating cancer
JOURNAL Patent: WO 0197843-A 838 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
SOURCE Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 320
AX355811/C 20 bp DNA linear PAT 06-FEB-2002
LOCUS AX355811
DEFINITION Sequence 839 from Patent WO0197843.
ACCESSION AX355811
VERSION AX355811.1 GI:18620479
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Method for enhancing antibody-induced cell lysis and creating cancer
JOURNAL Patent: WO 0197843-A 839 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
SOURCE Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 321
AX440125 20 bp DNA linear PAT 28-JUN-2002
LOCUS AX440125
DEFINITION Sequence 55 from Patent WO0173123.
ACCESSION AX440125
VERSION AX440125.1 GI:21664936
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor

JOURNAL Patent: WO 0173123-A 55 04-OCT-2001;
Nanosphere, Inc. (US)

FEATURES
SOURCE Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 322
AX440140 20 bp DNA linear PAT 28-JUN-2002
LOCUS AX440140
DEFINITION Sequence 70 from Patent WO0173123.
ACCESSION AX440140
VERSION AX440140.1 GI:21664951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 70 04-OCT-2001;
Nanosphere, Inc. (US)

FEATURES
SOURCE Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 323
AX465311 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX465311
DEFINITION Sequence 55 from Patent WO0218643.
ACCESSION AX465311
VERSION AX465311.1 GI:21899674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchhoff, J.J., Elghanian, R., Taton, T.A., Garmella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0218643-A 55 07-MAR-2002;
Nanosphere, Inc. (US)

FEATURES
SOURCE Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"


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/note="random synthetic sequence"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
1 AAAAAAAAAAAAAAAAAA 18
Db

RESULT 324
AX465326 20 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 70 from Patent WO0218643.
AX465326
ACCESSION AX465326.1 GI:21899689
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Markin,C.A., Letsinger,R.L., Mucic,R.C., Strohoff,J.J.,
Eghannian,R., Jacon,T.A., Garimella,V., Li,Z. and Park,S.J.
Nanoparticles having oligonucleotides attached thereto and uses
therefor
Patent: WO 0218643-A 70 07-MAR-2002;
JOURNAL Nanosphere, Inc. (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
1 AAAAAAAAAAAAAAAAAA 18
Db

RESULT 325
AX524879/c 20 bp DNA linear PAT 21-NOV-2002
LOCUS
DEFINITION Sequence 8 from Patent EP1236806.
AX524879
ACCESSION AX524879.1 GI:25169966
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Maruyama,T., Ishiguro,T. and Taya,T.
TITLE Oligonucleotide and method for detecting verotoxin
JOURNAL Patent: EP 1236806-A 8 04-SEP-2002;
Tosoh Corporation (JP)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
VT2 RNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 831 ATCAGCGCGGTTTGAC 848
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Db 20 ATCAGCGCGGTTTGAC 3

RESULT 326
AX547087/c 20 bp DNA linear PAT 01-MAR-2003
LOCUS
DEFINITION Sequence 226 from Patent WO02053141.
AX547087
ACCESSION AX547087
VERSION AX547087.1 GI:25912231
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 226 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
20 AAAAAAAAAAAAAAAAAA 3
Db

RESULT 327
AX547417/c 20 bp DNA linear PAT 01-MAR-2003
LOCUS
DEFINITION Sequence 556 from Patent WO02053141.
AX547417
ACCESSION AX547417
VERSION AX547417.1 GI:25812561
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 556 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
20 AAAAAAAAAAAAAAAAAA 3
Db

RESULT 328
AX547421 20 bp DNA linear PAT 01-MAR-2003
LOCUS
DEFINITION Sequence 560 from Patent WO02053141.
AX547421
ACCESSION AX547421
VERSION AX547421.1 GI:25812565
KEYWORDS
SOURCE
synthetic construct
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ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 560 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 329
AX556124 20 bp DNA linear PAT 27-NOV-2002
LOCUS AX556124
DEFINITION Sequence 55 from Patent WO0246472.
ACCESSION AX556124
VERSION AX556124.1 GI:25899506
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Minkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Tacon, T.A., Garimella, V., Li, Z., and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
JOURNAL Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 330
AX556139 20 bp DNA linear PAT 27-NOV-2002
LOCUS AX556139
DEFINITION Sequence 70 from Patent WO0246472.
ACCESSION AX556139
VERSION AX556139.1 GI:25899521
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Minkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Tacon, T.A., Garimella, V., Li, Z., and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
JOURNAL Patent: WO 0246472-A 70 13-JUN-2002;
Nanosphere, Inc. (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 331
AX664307 20 bp DNA linear PAT 22-MAR-2003
LOCUS AX664307
DEFINITION Sequence 5 from Patent WO0246398.
ACCESSION AX664307
VERSION AX664307.1 GI:29164237
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Willson, R.C. and Murphy, J.C.
TITLE Nucleic acid separation using immobilized metal affinity
JOURNAL Chromatography
Patent: WO 0246398-A 5 13-JUN-2002;
The University of Houston System (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 332
AX664308 20 bp DNA linear PAT 22-MAR-2003
LOCUS AX664308
DEFINITION Sequence 6 from Patent WO0246398.
ACCESSION AX664308
VERSION AX664308.1 GI:29164238
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Willson, R.C. and Murphy, J.C.
TITLE Nucleic acid separation using immobilized metal affinity
JOURNAL Chromatography
Patent: WO 0246398-A 6 13-JUN-2002;
The University of Houston System (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 333
AX708893 20 bp DNA linear PAT 04-APR-2003
LOCUS AX708893
DEFINITION Sequence 75 from Patent WO02101045.
ACCESSION AX708893
VERSION AX708893.1 GI:29564623
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Novartis AG (CH) ; IRM LLC (BM)
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 722 GTTTGCTGCTGCTGCTG 739
|||||
Db 3 GTTTGCTGCTGCTGCTG 20

RESULT 334
AX741040/c 20 bp DNA linear PAT 10-MAY-2003
LOCUS AX741040
DEFINITION Sequence 14 from Patent WO03027328.
ACCESSION AX741040
VERSION AX741040.1 GI:30523901
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 335
AX741052 20 bp DNA linear PAT 10-MAY-2003
LOCUS AX741052
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 336
BD008523 20 bp DNA linear PAT 31-JAN-2002
LOCUS BD008523
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial infections.
ACCESSION BD008523
VERSION BD008523.1 GI:18636896
KEYWORDS JP 2001503969-A/26.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
GENESIS RESEARCH & DEVELOPMENT CO LTD
OS Unidentified
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI
LINDA M SCOTT,
PI
ROSS L PRESTIGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
Location/Qualifiers
1. .20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 20;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 337
BD080522/c 20 bp RNA linear PAT 27-AUG-2002

LOCUS BD080522
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION BD080522
VERSION BD080522.1 GI:22626125
KEYWORDS JP 2001515087-A/1.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 20)
Pitsch,S., Weiss,P.A. and Jenny,L.
Ribonucleoside-derivative and method for preparing the same
Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PP 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH
Key
FT source Location/Qualifiers
1..20
/organism='Artificial Sequence'.
1..20
/location='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 338
BD107450/c 20 bp DNA linear PAT 18-SEP-2002

LOCUS BD107450
DEFINITION Method of detecting single base polymorphism.
ACCESSION BD107450
VERSION BD107450.1 GI:23202268
KEYWORDS UP 2002034599-A/9.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 20)
Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
Method of detecting single base polymorphism
Patent: JP 2002034599-A 9 05-FEB-2002;
TOYOBO CO LTD
OS Artificial Sequence
PN JP 2002034599-A/9
PD 05-FEB-2002
PP 26-JUL-2000 JP 2000225354
PI MASAYA SEGAWA,HITOSHI TAKARADA,TOSHIYA AONO,SATOKO YOSHIGA PC
C12Q1/68,C12M15/09,C12M15/00
CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
1..20
FT source

FT Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 339
BD174543/c 20 bp DNA linear PAT 18-MAR-2003

LOCUS BD174543
DEFINITION Oligonucleotide for detecting Vero toxin and detection method.
ACCESSION BD174543
VERSION BD174543.1 GI:29120233
KEYWORDS JP 2002253257-A/8.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 20)
Maruyama,T., Ishiguro,T. and Taya,T.
Oligonucleotide for detecting Vero toxin and detection method
Patent: JP 2002253257-A 8 10-SEP-2002;
TOSOH CORP
OS Artificial Sequence
PN JP 2002253257-A/8
PD 10-SEP-2002
PP 02-MAR-2001 JP 2001058143
PI TAKAHIRO MARUYAMA,TAKAHITO ISHIGURO,TOSHITAKA TAYA PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Oligonucleotide capable of binding specifically to VT2 RNA FH Key
FT source Location/Qualifiers
1..20
/organism='Artificial Sequence'.
1..20
/location='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 831 ATCAGCGCGGTGGAC 848
DB 20 ATCAGCGCGGTGGACC 3

RESULT 340
AR080294 21 bp DNA linear PAT 31-AUG-2000

LOCUS AR080294
DEFINITION Sequence 13 from patent US 5968754.
ACCESSION AR080294
VERSION AR080294.1 GI:10007029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Mammaglobin, a mammary-specific breast cancer protein
Patent: US 5968754-A 13 19-OCT-1999;
Location/Qualifiers
1..21
/organism='unknown'

/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 341
AR084521 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084521
DEFINITION Sequence 10 from patent US 5981185.
ACCESSION AR084521
VERSION AR084521.1 GI:10011292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 10 09-NOV-1999;
FEATURES Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAAAAA 18

RESULT 342
AR084524/c 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084524
DEFINITION Sequence 13 from patent US 5981185.
ACCESSION AR084524
VERSION AR084524.1 GI:10011295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 13 09-NOV-1999;
FEATURES Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 343
AR093143 21 bp DNA linear PAT 08-SEP-2000
LOCUS AR093143
DEFINITION Sequence 12 from patent US 5998596.
ACCESSION AR093143
VERSION AR093143.1 GI:10019895

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Bergan,R. and Neckers,L.
TITLE Inhibition of protein kinase activity by aptameric action of oligonucleotides
JOURNAL Patent: US 5998596-A 12 07-DEC-1999;
FEATURES Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 344
AR095412/c 21 bp DNA linear PAT 08-SEP-2000
LOCUS AR095412
DEFINITION Sequence 13 from patent US 6004756.
ACCESSION AR095412
VERSION AR095412.1 GI:10023262
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Method for detecting the presence of breast cancer by detecting an increase in mamaglobin mRNA expression
JOURNAL Patent: US 6004756-A 13 21-DEC-1999;
FEATURES Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 345
AR103542 21 bp DNA linear PAT 14-FEB-2001
LOCUS AR103542
DEFINITION Sequence 66 from patent US 6087485.
ACCESSION AR103542
VERSION AR103542.1 GI:12815130
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brooke-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M., Miller,A. and North,M.
TITLE Aschma related genes
JOURNAL Patent: US 6087485-A 66 11-JUL-2000;
FEATURES Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1225 CTCCTCTCTCTAGCTCTCTC 1244
Db 1 CTCCTCTCTCTCTCTCTCTC 20

RESULT 346
LOCUS AR118155 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6140489.
ACCESSION AR118155
VERSION AR118155.1 GI:14099061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brenner,S.
TITLE Compositions for sorting polynucleotides
JOURNAL Patent: US 6140489-A 23 31-OCT-2000;
FEATURES
Source 1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 347
LOCUS AR153849 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6238624.
ACCESSION AR153849
VERSION AR153849.1 GI:15121902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller,M.J., Tu,B., Evans,G.A. and Sosnowski,R.G.
TITLE Methode for transport in molecular biological analysis and
JOURNAL Patent: US 6238624-A 2 29-MAY-2001;
FEATURES
Source 1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 348
LOCUS BD224108 21 bp DNA linear PAT 17-JUL-2003
DEFINITION Mammaglobin, breast cancer secretory protein specific to mamma.
ACCESSION BD224108
VERSION BD224108.1 GI:33033878
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, breast cancer secretory protein specific to mamma
JOURNAL Patent: JP 2002525098-A 10 13-AUG-2002;
WASHINGTON UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2002525098-A/10
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572241
PR 29-SEP-1998 US 09/162622
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
C12N15/00
CC Description of Artificial Sequence:Synthetic
FH Key Location/Qualifiers
FT source 1. .21
FT location/Qualifiers
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 349
LOCUS CO846797 21 bp RNA linear PAT 02-AUG-2004
DEFINITION Sequence 46 from Patent WO2004036221.
ACCESSION CO846797
VERSION CO846797.1 GI:50895947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS O'Toole,M.M. and Liu,W.
TITLE Compositions and methods for diagnosing and treating autoimmune
JOURNAL disease
Patent: WO 2004036221-A 46 29-APR-2004;
Wyleth (US); O'Toole, Margot Mary (US); Liu, Wei (US)
FEATURES
Source 1. .21
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 981 CGCGGACGCTTCTGTTTC 998
Db 3 CGCGTGAAGTTCATGTTTC 20

RESULT 350
LOCUS I36166 21 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 2 from patent US 5605662.
ACCESSION I36166
VERSION I36166.1 GI:2086679

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller, M.J. and Tu, B.
TITLE Active programmable electronic devices for molecular biological
JOURNAL analysis and diagnostics
PATENT: US 5605662-A 2 25-FEB-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 351
165744/c 165744 21 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 13 from patent US 5668267.
ACCESSION 165744
VERSION 165744.1 GI:2482314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Polynucleotides encoding mammaglobin, a mammary-specific breast
JOURNAL cancer protein
PATENT: US 5668267-A 13 16-SEP-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 352
184433/c 184433 21 bp DNA linear PAT 04-APR-1998
LOCUS Sequence 23 from patent US 5695934.
ACCESSION 184433
VERSION 184433.1 GI:3021953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brenner, S.
TITLE Massively parallel sequencing of sorted polynucleotides
JOURNAL Patent: US 5695934-A 23 09-DEC-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 353
AR322245/c AR322245 21 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 13 from patent US 6566072.
ACCESSION AR322245
VERSION AR322245.1 GI:33707814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6566072-A 13 20-MAY-2003;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 354
AR452591/c AR452591 21 bp mRNA linear PAT 20-FEB-2004
LOCUS Sequence 13 from patent US 6677428.
ACCESSION AR452591
VERSION AR452591.1 GI:42684381
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6677428-A 13 13-JAN-2004;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="mRNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 355
AX104720/c AX104720 21 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 912 from Patent WO0122972.
ACCESSION AX104720
VERSION AX104720.1 GI:13920917
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Kriegl, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 912 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 356
LOCUS AX355812 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 840 from Patent WO0197843.
ACCESSION AX355812
VERSION AX355812.1 GI:18620480
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Method for enhancing antibody-induced cell lysis and treating
Cancer
JOURNAL Patent: WO 0197843-A 840 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 357
LOCUS AX547773 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 912 from Patent WO02053141.
ACCESSION AX547773
VERSION AX547773.1 GI:25812917
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 912 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 358
LOCUS AX825123 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 21 from Patent WO03072818.
ACCESSION AX825123
VERSION AX825123.1 GI:39750852
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 21 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_molecy="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
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modified_base 9
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modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
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modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 359
LOCUS AX825124 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 22 from Patent WO03072818.
ACCESSION AX825124
VERSION AX825124.1 GI:39750853
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences


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REFERENCE
1      artificial sequences.
AUTHORS
1      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE
1      Method for sorting single-stranded nucleic acids
JOURNAL
1      Patent: WO 03072818-A 22 04-SEP-2003,
1      Degussa Bioactives GmbH (DE)
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
modified_base
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/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
RESULT 360
AX825125/C
LOCUS
1      AX825125
21 bp DNA linear PAT 11-DEC-2003
DEFINITION
1      Sequence 23 from Patent WO03072818.
ACCESSION
1      AX825125
VERSION
1      AX825125.1 GI:39750854
KEYWORDS
1
SOURCE
1      synthetic construct
1      synthetic construct
1      artificial sequences.
REFERENCE
1
AUTHORS
1      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE
1      Method for sorting single-stranded nucleic acids
JOURNAL
1      Patent: WO 03072818-A 23 04-SEP-2003,
1      Degussa Bioactives GmbH (DE)
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Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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modified_base
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/mod_base=OTHER
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
RESULT 361
AX825126/C
LOCUS
1      AX825126
21 bp DNA linear PAT 11-DEC-2003
DEFINITION
1      Sequence 24 from Patent WO03072818.
ACCESSION
1      AX825126
VERSION
1      AX825126.1 GI:39750855
KEYWORDS
1
SOURCE
1      synthetic construct
1      synthetic construct
1      artificial sequences.
REFERENCE
1
AUTHORS
1      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE
1      Method for sorting single-stranded nucleic acids
JOURNAL
1      Patent: WO 03072818-A 24 04-SEP-2003,
1      Degussa Bioactives GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
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RESULT 362
AX825127/c
LOCUS AX825127 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 25 from Patent WO03072818.
ACCESSION AX825127
VERSION AX825127.1 GI:39750856
KEYWORDS
SOURCE .
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 25 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kuenstlichen
        Sequenz:Capture-Oligonukleotid"
misc_binding 1
            /bound_moiety="Biotin"
modified_base 3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 9
            /note="LNA-T (Locked Nucleic Acid)"
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modified_base 12
            /note="LNA-T (Locked Nucleic Acid)"
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modified_base 15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 18
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modified_base
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            /mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No.1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 363
AX825128/c
LOCUS AX825128 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 26 from Patent WO03072818.
ACCESSION AX825128
VERSION AX825128.1 GI:39750857
KEYWORDS
SOURCE .
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 26 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
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            /bound_moiety="Biotin"
modified_base 3
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            /mod_base=OTHER
modified_base 6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 9
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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No.1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 364
AX825129/c
LOCUS AX825129 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 27 from Patent WO03072818.
ACCESSION AX825129
VERSION AX825129.1 GI:39750858
KEYWORDS
SOURCE .
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 27 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Beschreibung der kuenstlichen
        Sequenz:Capture-Oligonukleotid"
misc_binding 1
            /bound_moiety="Biotin"
modified_base 3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base 9
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modified_base 12
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modified_base 15
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Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 365
AX825130/c      AX825130      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 28 from Patent WO03072818.
ACCESSION      AX825130
VERSION      AX825130.1 GI:39750859
KEYWORDS
SOURCE      . synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 28 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
              Location/Qualifiers
FEATURES
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              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_moiety="Biotin"
  modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
  modified_base 6
              /mod_base=OTHER
  modified_base 9
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  modified_base 12
              /note="LNA-T (Locked Nucleic Acid)"
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Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 366
AX825131/c      AX825131      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 29 from Patent WO03072818.
ACCESSION      AX825131
VERSION      AX825131.1 GI:39750860
KEYWORDS
SOURCE      . synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
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REFERENCE      1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 29 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
              Location/Qualifiers
FEATURES
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              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_moiety="Biotin"
  modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
  modified_base 6
              /mod_base=OTHER
  modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
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  modified_base 12
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  modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
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              /mod_base=OTHER

Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 367
AX825132/c      AX825132      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 30 from Patent WO03072818.
ACCESSION      AX825132
VERSION      AX825132.1 GI:39750861
KEYWORDS
SOURCE      . synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 30 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
              Location/Qualifiers
FEATURES
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              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_moiety="Biotin"
  modified_base 3
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  modified_base 6
              /mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid) "
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15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAA 1

RESULT 368
AX825133/c AX825133 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 31 from Patent WO03072818.
DEFINITION AX825133
ACCESSION AX825133.1 GI:39750862
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 31 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers

1. .21
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/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAA 1

RESULT 369
AX825134/c AX825134 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 32 from Patent WO03072818.
DEFINITION AX825134
ACCESSION AX825134
VERSION AX825134.1 GI:39750863
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 32 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers

1. .21
/organism="synthetic construct"
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/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAA 1

RESULT 370
AX825139/c AX825139 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 37 from Patent WO03072818.
DEFINITION AX825139
ACCESSION AX825139
VERSION AX825139.1 GI:39750868
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 37 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source location/Qualifiers

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/note="Beschreibung der kuenstlichen

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	9	/mod_base=OTHER
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	12	/mod_base=OTHER
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	15	/mod_base=OTHER
	modified_base	/note="LNA-T (Locked Nucleic Acid)"
	18	/mod_base=OTHER
	Query Match	1.1%; Score 14.8; DB 1; Length 21;
	Beet Local Similarity	88.9%; Pred.No.1.7e+02;
	Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Oy	1520 AAAAAAAAAAGTAAA 1537	
Db	18 AAAAAAAAAAAAAAAAAA 1	
RESULT 371		
LOCUS	AX825140	21 bp DNA linear PAT 11-DEC-2003
DEFINITION	Sequence 38 from Patent WO03072818.	
ACCESSION	AX825140	
VERSION	AX825140.1 GI:39750869	
KEYWORDS		
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
REFERENCE	artificial sequences.	
AUTHORS	1 Bockenkamp,D., Dieck,T.H. and Hoppe,H.U.	
TITLE	Method for sorting single-stranded nucleic acids	
JOURNAL	Patent: WO 03072818-A 38 04-SBP-2003;	
DEGUSA	Degussa Bioactives GmbH (DE)	
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	/mod_base=OTHER	
	9	
	/note="LNA-T (Locked Nucleic Acid)"	
	/mod_base=OTHER	
	12	
	/note="LNA-T (Locked Nucleic Acid)"	
	/mod_base=OTHER	
	15	
	/note="LNA-T (Locked Nucleic Acid)"	
	/mod_base=OTHER	
	18	
	/note="LNA-T (Locked Nucleic Acid)"	
	/mod_base=OTHER	

Query Match	1.1%;	Score 14.8;	DB 1;	Length 21;
Best Local Similarity	88.9%;	Pred. No. 1.7e+02;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	1520	AAAAAAAAAAGTAA	1537	
Db	18	AAAAAAAAAAAAAAAA	1	
RESULT 372				
AX825141/c				
LOCUS	AX825141	21 bp	DNA	linear
DEFINITION	Sequence 39 from Patent WO03072818.			PAT 11-DEC-2003
ACCESSION	AX825141			
VERSION	AX825141.1	GI:39750870		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1			
TITLE	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
JOURNAL	Method for sorting single-stranded nucleic acids			
DEGUSSES	Patent: WO 03072818-A 39 04-SEP-2003;			
DEGUSSES	Degussa Bioactives GmbH (DE)			
FEATURES				
source	Location/Qualifiers			
	1..21			
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
	/note="Beschreibung der kuenstlichen			
	Sequenz:Capture-Oligonukleotid"			
	1			
	/bound_moiety="Biotin"			
	3			
	/note="LNA-T (Lockedd Nucleic Acid)"			
	6			
	/mod_base=OTHER			
	modified_base			
	9			
	/note="LNA-T (Lockedd Nucleic Acid)"			
	12			
	/mod_base=OTHER			
	modified_base			
	15			
	/note="LNA-T (Lockedd Nucleic Acid)"			
	18			
	/mod_base=OTHER			
	modified_base			
	18			
	/note="LNA-T (Lockedd Nucleic Acid)"			
	/mod_base=OTHER			
	Query Match	1.1%;	Score 14.8;	DB 1;
	Best Local Similarity	88.9%;	Pred. No. 1.7e+02;	
	Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;
	Gaps 0;			
OY	1520	AAAAAAAAAAGTAA	1537	
Db	18	AAAAAAAAAAAAAAAA	1	
RESULT 373				
AX825142/c				
LOCUS	AX825142	21 bp	DNA	linear
DEFINITION	Sequence 40 from Patent WO03072818.			PAT 11-DEC-2003
ACCESSION	AX825142			
VERSION	AX825142.1	GI:39750871		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1			
TITLE	synthetic construct			
JOURNAL	synthetic construct			
DEGUSSES	artificial sequences.			

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 40 04-SEP-2003;
Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 374
AX825143/C 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 41 from Patent WO03072818.
ACCESSION AX825143
VERSION AX825143.1 GI:39750872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 41 04-SEP-2003;
Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 375
AX825144/C 21 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 42 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 42 04-SEP-2003;
Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 376

```

AX825145/c  AX825145  21 bp  DNA  linear  PAT 11-DEC-2003
LOCUS      Sequence 43 from Patent WO03072818.
ACCESSION  AX825145
VERSION    AX825145.1  GI:39750874
KEYWORDS
SOURCE     .
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL    Patent: WO 03072818-A 43 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES   Location/Qualifiers
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"
misc_binding
            1
            /bound_moiety="Biotin"
modified_base
            3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base
            6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base
            9
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base
            12
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base
            15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
modified_base
            18
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy  1520 AAAAAAAAAAGTAAA 1537
Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 377
AX825146/c  AX825146  21 bp  DNA  linear  PAT 11-DEC-2003
LOCUS      Sequence 44 from Patent WO03072818.
ACCESSION  AX825146
VERSION    AX825146.1  GI:39750875
KEYWORDS
SOURCE     .
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL    Patent: WO 03072818-A 44 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES   Location/Qualifiers
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"

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misc_binding      1
                  /bound_moiety="Biotin"
modified_base     3
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     6
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     9
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    12
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    15
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    18
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy  1520 AAAAAAAAAAGTAAA 1537
Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 378
AX825147/c  AX825147  21 bp  DNA  linear  PAT 11-DEC-2003
LOCUS      Sequence 45 from Patent WO03072818.
ACCESSION  AX825147
VERSION    AX825147.1  GI:39750876
KEYWORDS
SOURCE     .
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL    Patent: WO 03072818-A 45 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES   Location/Qualifiers
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"
misc_binding      1
                  /bound_moiety="Biotin"
modified_base     3
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     6
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     9
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    12
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    15
                  /note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    18
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                  /mod_base=OTHER

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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 379
AX825148/c. 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825148
DEFINITION Sequence 46 from Patent WO03072818.
ACCESSION AX825148
VERSION AX825148.1 GI:39750877
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 46 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
/mod_base=OTHER

modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
/note="LNA-T (Locked Nucleic Acid) "

modified_base
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 380
AX825149/c. 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825149
DEFINITION Sequence 47 from Patent WO03072818.
ACCESSION AX825149
VERSION AX825149.1 GI:39750878
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.

TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 47 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
/mod_base=OTHER

modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
/mod_base=OTHER

modified_base
/note="LNA-T (Locked Nucleic Acid) "

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 381
AX825150/c. 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825150
DEFINITION Sequence 48 from Patent WO03072818.
ACCESSION AX825150
VERSION AX825150.1 GI:39750879
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 48 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
/mod_base=OTHER

modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
/mod_base=OTHER

modified_base
/note="LNA-T (Locked Nucleic Acid) "


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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 382
AX825156/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825156
DEFINITION Sequence 54 from Patent WO03072818.
ACCESSION AX825156
VERSION AX825156.1 GI:39750885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 54 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

RESULT 383
AX825157/c
```

```
LOCUS AX825157 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 55 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

RESULT 384
AX825158/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825158
DEFINITION Sequence 56 from Patent WO03072818.
ACCESSION AX825158
VERSION AX825158.1 GI:39750887
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 56 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
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modified_base
3 /bound_moiety="Biotin"
/ note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
6 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
9 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
12 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
15 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
18 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
21 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER

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Query Match	1.1%	Score 14.8;	DB 1;	Length 21;
Best Local Similarity	88.9%	Pred. No. 1.7e+02;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      1520 AAAAAAAAAAAGTAAA 1537
          |||||
Db      19  AAAAAAAAAAAAAAA 2

```

RESULT	385
AX825160/c	
LOCUS	AX825160 21 bp DNA linear PAT 11-DEC-2003
DEFINITION	Sequence 58 from Patent WO03072818.
ACCESSION	AX825160
VERSION	AX825160.1 GI:39750889
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.

REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 56 04-SEP-2003;
DEGUS	DEGUSa Bioactives GmbH (DE)
FEATURES	Location/Qualifiers
source	1..21

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misc_binding      1 /aqueousTemperature=degCelsius=298.15
modified_base     3 /bound_molecule="Biotin"
                  3 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER
modified_base     6 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER
modified_base     9 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER
modified_base    12 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER
modified_base    15 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER
modified_base    18 /note="LNA-T (locked Nucleic Acid) "
                  /mod_base=OTHER

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Query Match	1,18; Score 14,8; DB 1; Length 21;
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Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGCTAAA 1537
   |||||
Db 19 AAAAAAAAAAAAAAAAAA 2

```

RESULT	386		
AX825161/c			
LOCUS	AX825161	21 bp	DNA
DEFINITION	Sequence 59 from Patent WO03072818.		linear
			PAT 11-DEC-2003

ORGANISM	synthetic construct artificial sequences.
REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 59 04-SEP-2003;
DEPOSIT	Degussa Bioactives GmbH (DE)
FEATURES	Location/Qualifiers

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misc_binding 1
/bound_moiety="Biotin"
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```

/Note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified base 6

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- /note="LNA-T (Locked Nucleic Acid)"
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modified_base
9

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/mod_base=OTHER
modified_base
12
/notes="RNA-T (locked Nucleic Acid)"

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modified_base
15
/note="LNA-T (Locked Nucleic Acid)"

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modified_base
18
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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Best Local Similarity	88.9%	Pred. No. 1.7e+02;		
Matches	16;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	1520	AAAAAAAAAAAGTAAA	1537
D5	19	AAAAAAAAAAAAA	2

RESULT	387		
AX825162/c			
LOCUS	AX825162	21 bp	DNA
DEFINITION	Sequence	60 from Patent WO03072818.	linear
ACCESSION	AX825162		
VERSION	AX825162.1	GI:39750891	
KEYWORDS			
SOURCE			
	synthetic construct		

REFERENCE	
AUTHORS	1
TITLE	artificial sequences.
	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
	Method for sorting single-stranded nucleic acids

JOURNAL Patent: WO 03072818-A 60 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
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modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
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modified_base 18
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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAA 2

RESULT 388
AX825164/c
LOCUS AX825164 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 62 from Patent WO03072818.
ACCESSION AX825164
VERSION AX825164.1 GI:39750893
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 62 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
/mod_base=OTHER

modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
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modified_base 18
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modified_base 18
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3

RESULT 390
AX825166/c
LOCUS AX825166 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 63 from Patent WO03072818.
ACCESSION AX825166
VERSION AX825166.1 GI:39750894
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 63 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source 1..21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid) "

modified_base 6
/mod_base=OTHER

modified_base 9
/note="LNA-T (Locked Nucleic Acid) "

modified_base 12
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
/mod_base=OTHER

modified_base 18
/note="LNA-T (Locked Nucleic Acid) "

modified_base 18
/mod_base=OTHER

DEFINITION Sequence 64 from Patent WO03072818.
ACCESSION AX825166
VERSION AX825166.1 GI:39750895
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequence.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 64 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
 Location/Qualifiers
FEATURES
source 1..21
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen
 Sequenz: Capture-Oligonukleotid"
misc_binding 1
 /bound_moiety="Biotin"
modified_base 3
 /note="TNA-T (locked Nucleic Acid) "
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 /note="TNA-T (locked Nucleic Acid) "
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modified_base 9
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 /mod_base=OTHER
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modified_base 15
 /note="TNA-T (locked Nucleic Acid) "
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modified_base 18
 /note="TNA-T (locked Nucleic Acid) "
 /mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAAAAAAAAAAAAA 4
RESULT 391
BD080832/c 21 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION BD080832
VERSION BD080832.1 GI:22626435
KEYWORDS
SOURCE unidentifed
ORGANISM unidentifed
 unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary specific breast cancer protein
JOURNAL Patent: JP 2001516569-A 10 02-OCT-2001;
 WASHINGTON UNIVERSITY
COMMENT
OS Unidentifed
PN JP 2001516569-A/10
PD 02-OCT-2001
PF 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
PC A61P35/00,
PC C07K14/47,C12N15/00

CC Strandedness: Single;
CC Topology: Linear;
CC Mammaglobin, a secreted mammary specific breast cancer protein
FH Key Location/Qualifiers
FT source 1..21
 /organism='Unidentifed'.
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source 1..21
 /organism="unidentifed"
 /mol_type="genomic DNA"
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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAAAAAAAAAAAAA 4
RESULT 392
BD087491 21 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Self-assembling microelectronic integration system capable of
 designating self address, compartment device, mechanism, method and
 operation for molecular biological analysis and diagnosis.
ACCESSION BD087491 GI:22633101
VERSION BD087491.1 GI:22633101
KEYWORDS JP 2001525193-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequence.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
 Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
 designating self address, compartment device, mechanism, method and
 operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 2 11-DEC-2001;
 NANOGEN INC
COMMENT
OS Artificial Sequence
PN JP 2001525193-A/2
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
 NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthesized with v at 3'
CC termilus to
CC provide ribonucleic acid base for reactivity; Poly A sequence
CC for reduced
CC secondary structure
FH key Location/Qualifiers
FT source 1..21
 /organism='Artificial Sequence'.
FEATURES
source 1..21
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAAAAA 18

[illegible]

RESULT	395	ARI47331/c	19 bp	DNA	linear	PAT	08-AUG-2001
LOCUS	ARI47331						
DEFINITION	Sequence 6 from patent US 6221584.						
ACCESSION	ARI47331						
VERSION	ARI47331.1	GI:15111134					
KEYWORDS	.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 19)						
AUTHORS	Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.						
TITLE	Method of detecting telomerase activity						
JOURNAL	Patent: US 6221584-A 6 24-Apr-2001;						
FEATURES	Location/Qualifiers						
source	1..19						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	1.0%; Score 14.6; DB 1;						
Best Local Similarity	78.9%; Pred. No.2.2e+02;						
Matches	15, Conservative	2; Mismatches	2; Indels	0; Gaps	0;		
CY	1518 TTTAAAAAAAAAAGTTAA	1536					
Db	19 DKAAAAAAAAAAAAAAAAAAAA	1					
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RESULT	396						
AX825107							
LOCUS	AX825107	21 bp	DNA	linear	PAT	11-DEC-2003	
DEFINITION	Sequence 5 from Patent WO03072818.						
ACCESSION	AX825107						
VERSION	AX825107.1	GI:39750836					
KEYWORDS	.						
SOURCE	synthetic construct						
ORGANISM	synthetic construct						
	artificial sequences.						
REFERENCE	1						
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.						
TITLE	Method for sorting single-stranded nucleic acids						
JOURNAL	Patent: WO 03072818-A 5 04-SEP-2003;						
	Degussa Bioactives GmbH (DE)						
FEATURES	Location/Qualifiers						
source	1..21						
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	/db_xref="taxon:32630"						
	/note="Beschreibung der kuenstlichen						
	Sequenz:Capture-Oligonukleotid"						
	1						
	/bound_moiety="Biotin"						
	3						
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	6						
	/note="LNA-T (Locked Nucleic Acid)"						
	/mod_base=OTHER						
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	/note="LNA-T (Locked Nucleic Acid)"						
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	/note="LNA-T (Locked Nucleic Acid)"						
	/mod_base=OTHER						

Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1302 TCTATTGTTTATTTTCAGA 1332
Db 1 TTTTATTTTATTTTATTTTAGA 21

RESULT 397
AX825117 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825117
DEFINITION Sequence 15 from Patent WO03072818.
ACCESSION AX825117
VERSION AX825117.1 GI:39750846
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 15 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
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modified_base 6
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/mod_base=OTHER

modified_base 9
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modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
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Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1246 TCTTGTGTTGTTTATTC 1266
Db 1 TTTTATTTTATTTTATTC 21

RESULT 398
BD085544/c 22 bp RNA linear PAT 27-AUG-2002
LOCUS BD085544
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085544
VERSION BD085544.1 GI:22631154
KEYWORDS JP 2001333800-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 22)

AUTHORS Shimada, K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 1 04-DEC-2001;
UNITBEH CO LTD

COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/1
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAORI SHIMADA
PC C1201/68, C12N15/09, G01N33/50, C12N15/00
CC Method of comparison and detection of RNA amount and DNA amount

FEATURES
FH Key Location/Qualifiers
FT source 1..22
/organism="Homo sapiens (human)".
source 1..22
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1246 TCTTGTGTTGTTTATTC 1266
Db 21 TTTTATTTTATTTTATTC 1

RESULT 399
AX692829 25 bp DNA linear PAT 31-MAR-2003
LOCUS AX692829
DEFINITION Sequence 5561 from Patent EP1281758.
ACCESSION AX692829
VERSION AX692829.1 GI:29415792
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C. T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5561 05-FEB-2003;
Aecmica, Inc. (US)
FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.6; DB 1; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1512 TGTTAATTAAAAAAG 1532
Db 21 TCTCAAAAAAAG 1

RESULT 400
AR089217/c 17 bp DNA linear PAT 07-SEP-2000
LOCUS AR089217
DEFINITION Sequence 13 from patent US 5994061.
ACCESSION AR089217
VERSION AR089217.1 GI:10015974
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Tam,S.-P. and Zhang,X.
TITLE DNA constructs and method for screening for increased expression
JOURNAL of human apo A1 gene
FEATURES Patent: US 5994061-A 13 30-NOV-1999;
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 345 CTGCCGCCGCCGCCGAG 360
Db 16 CTGCCGCCGCCGCCGAG 1

RESULT 401
BD201511/c 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD201511.1 GI:33011281
VERSION JP 2002509721-A/4537.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
PATENT: JP 2002509721-A 4537 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/4537
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
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FEATURES
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/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1512 TGTTAATTAAAAAAA 1527
Db 17 TGTTAATTAAAAAAA 2

RESULT 402
BD201512/c 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION

ACCESSION BD201512
VERSION BD201512.1 GI:33011282
KEYWORDS JP 2002509721-A/4538.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
PATENT: JP 2002509721-A 4538 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/4538
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
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FEATURES
source 1..17
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/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1512 TGTTAATTAAAAAAA 1527
Db 16 TGTTAATTAAAAAAA 1

RESULT 403
BD258338 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor gene using nucleic acid molecules.
DEFINITION BD258338
ACCESSION BD258338.1 GI:33068108
VERSION JP 2002541795-A/6131.
KEYWORDS JP 2002541795-A/6131.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor gene using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6131 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/6131
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/128390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
PI C12N15/09,A61K38/00,A61K48/00,A61P3/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1.91),(C12P21/02, PC
C12R1.91),

PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1247 CTTTGTGTTGTTT 1262
|||||
2 CTTTGTGTTGTTT 17

RESULT 404
LOCUS BD258339 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258339
VERSION BD258339.1 GI:33068109
KEYWORDS JP 2002541795-A/6132.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6132 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6132
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1247 CTTTGTGTTGTTT 1262
|||||
1 CTTTGTGTTGTTT 16

RESULT 405
LOCUS CQ616719/C 17 bp DNA linear PAT 02-FEB-2004

DEFINITION Sequence 1459 from Patent WO0192524.
ACCESSION CQ616719
VERSION CQ616719.1 GI:41666937
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 1459 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 332 TTCCGAGAGCTCTG 347
|||||
16 TTCCGAGAGCTCTG 1

RESULT 407
LOCUS CQ617530/C 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2270 from Patent WO0192524.
ACCESSION CQ617530
VERSION CQ617530.1 GI:41667748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2270 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
Source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
Db 17 GCCGAGGCCCGCAGG 2

RESULT 408
LOCUS C0617531/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2271 from Patent WO0192524.
ACCESSION C0617531
VERSION C0617531.1 GI:41667749
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2271 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES Location/Qualifiers
Source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
Db 16 GCCGAGGCCCGCAGG 1

RESULT 409
LOCUS AR187057/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2545 from patent US 6346398.
ACCESSION AR187057
VERSION AR187057.1 GI:20233022
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2545 12-FEB-2002;
FEATURES Location/Qualifiers
Source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
Db 16 GCCGAGGCCCGCAGG 1

Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1521 AAAAAAAAAAGTAAA 1536
Db 17 AAAAAAAAAAGTAAA 2

RESULT 410
LOCUS AR285940/c 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 312 from patent US 6528640.
ACCESSION AR285940
VERSION AR285940.1 GI:29723536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpetsky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 312 04-MAR-2003;
FEATURES Location/Qualifiers
Source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 469 GGGGCGCGCGCTGAC 484
Db 17 GGGGCGCGCGCTGCC 2

RESULT 411
LOCUS AR323667/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1069 from patent US 6566127.
ACCESSION AR323667
VERSION AR323667.1 GI:33709475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1069 20-MAY-2003;
FEATURES Location/Qualifiers
Source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1521 AAAAAAAAAAGTAAA 1536
Db 17 AAAAAAAAAAGTAAA 2

RESULT 412
LOCUS AR397930/c 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 311 from patent US 6617438.
ACCESSION AR397930
VERSION AR397930.1 GI:40135323
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Beigelman, L., Burgin, A.B., Beaudry, A., Karpelsky, A.,
Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
JOURNAL Oligonucleotides with enzymatic activity
FEATURES Patent: US 6617438-A 311 09-SEP-2003;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 469 GGGGGCGCGCTGAC 484
DB 17 GGGGGCGCGCTGCC 2

RESULT 413
LOCUS AR457782/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1459 from patent US 6686188.
ACCESSION AR457782
VERSION AR457782.1 GI:42692839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES Predominantly in heart and muscle
Patent: US 6686188-A 1459 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 332 TTCCGAGAGCTCTG 347
DB 17 TTCCGAGAGCTGCTG 2

RESULT 414
LOCUS AR457783/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1460 from patent US 6686188.
ACCESSION AR457783
VERSION AR457783.1 GI:42692840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES Predominantly in heart and muscle
Patent: US 6686188-A 1460 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 332 TTCCGAGAGCTCTG 347
DB 16 TTCCGAGAGCTGCTG 1

RESULT 415
LOCUS AR458593/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2270 from patent US 6686188.
ACCESSION AR458593
VERSION AR458593.1 GI:42693650
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES Predominantly in heart and muscle
Patent: US 6686188-A 2270 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 GCCGAGGCCCGCAGG 411
DB 17 GCCGAGGCCCGCAGG 2

RESULT 416
LOCUS AR458594/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2271 from patent US 6686188.
ACCESSION AR458594
VERSION AR458594.1 GI:42693651
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES Predominantly in heart and muscle
Patent: US 6686188-A 2271 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 GCCGAGGCCCGCAGG 411
DB 16 GCCGAGGCCCGCAGG 1

RESULT 417
LOCUS AX674744 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 3189 from Patent WO03004526.

ACCESSION AX674744
VERSION AX674744.1 GI:29333092
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 3189 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
|||
2 ATCTTATTTCCCTT 17

RESULT 418
AX729555 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 1189 from Patent WO03025175.
ACCESSION AX729555
VERSION AX729555.1 GI:30508898
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1189 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
|||
2 ATCTTATTTCCCTT 17

RESULT 419
AX730083 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION Sequence 1717 from Patent WO03025175.
ACCESSION AX730083
VERSION AX730083.1 GI:30509426
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1717 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1315 TTTTCAGACAGATC 1330
|||||
16 TTTTCAGACAGATC 1

RESULT 420
AX761696 17 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION Sequence 5017 from Patent WO03040369.
ACCESSION AX761696
VERSION AX761696.1 GI:32256312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5017 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
|||
2 ATCTTATTTCCCTT 17

RESULT 421
A89378 18 bp DNA linear PAT 22-JAN-2000
LOCUS
DEFINITION Sequence 1526 from Patent WO9833904.
ACCESSION A89378
VERSION A89378.1 GI:6737948
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1526 06-AUG-1998;
BIOLOGISTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1. .18
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1312 TTATTTTCAGACAG 1327
Db 16 TTATTTTCAGACAG 1

RESULT 422
LOCUS AR106885 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 46 from patent US 6107092.
ACCESSION AR106885
VERSION AR106885.1 GI:12821415
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 46 22-AUG-2000;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1491 ACATTATTCAGAAA 1506
Db 18 AGATTATTCAGAAA 3

RESULT 423
LOCUS AX662307 18 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 46 from Patent WO02059293.
ACCESSION AX662307
VERSION AX662307.1 GI:29163190
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Forster,A.C. and Blacklow,S.C.
TITLE Process and compositions for peptide, protein and peptidomimetic synthesis
JOURNAL Patent: WO 02059293-A 46 01-AUG-2002;
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="FROM SYNTHETIC DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1514 TTAATTAATAAAAAA 1529
Db 16 TGAATTAATAAAAAA 1

RESULT 424

BD066891/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD066891
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066891
VERSION BD066891.1 GI:22612494
KEYWORDS JP 2001511000-A/1526.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1526 07-AUG-2001;
COMMENT BIOLOGIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1526
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH key
FEATURES
source FT
FT source 1..18
/organism="Unknown".
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1312 TTATTTTCAGACAG 1327
Db 16 TTATTTTCAGACAG 1

RESULT 425
LOCUS BD096088 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Rice peroxidase having various characteristics.
ACCESSION BD096088
VERSION BD096088.1 GI:22641676
KEYWORDS WO 0142475-A/27.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Ohashi,Y., Mitsuhashi,I., Sasaki,T., Nagamura,Y., It,H., Iwai,T. and Hiraga,S.
TITLE Rice peroxidase having various characteristics
JOURNAL Patent: WO 0142475-A 27 14-JUN-2001;
FORESTRY AND FISHERIES NATIONAL INSTITUTE OF AGRICULTURE
RESOURCES, KENICHI NOGUCHI YUKO OHASHI, ICHIRO MITSUHASHI, TAKUJI SASAKI, YOSHIKI NAGAMURA, HIROYUKI ITO, TAKAYOSHI IMAI, SUSUNU HIRAGA
OS Oryza sativa (rice)
PN WO 0142475-A/27
PD 14-JUN-2001
PF 08-DEC-2000 WO 2000JP008728
PR 10-DEC-1999 JP 99P 352472
PI YUKO OHASHI, ICHIRO MITSUHASHI, TAKUJI SASAKI, YOSHIKI NAGAMURA, HIROYUKI ITO, TAKAYOSHI IMAI, SUSUNU HIRAGA
PC C12N15/53, C12N9/08, C12Q1/68
CC R1420FPI
FH key
Location/Qualifiers

FT source 1.18
/organism='Oryza sativa (rice)'.
FEATURES
source 1.18
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 669 TCACCTCTGACGCCGC 684
|||||
2 TCACCTCTGACGCCGC 17

RESULT 426
A40129/c A40129 20 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 5 from Patent WO9423026.
DEFINITION A40129
ACCESSION A40129
VERSION A40129.1 GI:2296287
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Vasseur M., Blumenfeld M., Megueni S. and Poddevin B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND APPLICATIONS
JOURNAL Patent: WO 9423026-A 5 13-OCT-1994;
GENSET (FR)
COMMENT Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES
source 1.20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1302 TCTATTTTATTT 1317
|||||
16 TCTATTTTATTTT 1

Db 16 TCTATTTTATTTT 1

RESULT 427
BD244919 20 bp DNA linear PAT 17-JUL-2003
LOCUS BD244919
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244919
VERSION BD244919.1 GI:33054689
KEYWORDS JP 2002528391-A/47.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Beesterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 47 03-SEP-2002;
METHYGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/47
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN, ALAN ROBERT MACLEOD, WILLIAM M SIDERS PC
A61K48/00, A61K31/165, A61K31/19, A61K31/513, A61K31/517, A61K31/PC
706,

PC A61K31/7068, A61K31/7088, A61K31/7125, A61K45/00, A61P35/00, C12N15/PC
09//
PC C12N5/10, C12N15/00, C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1.20
/organism='Artificial Sequence'.
FEATURES
source 1.20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 726 TGCCTGTGCTGCTGCC 741
|||||
4 TGCCTGTGCTGCTGCC 19

Db 4 TGCCTGTGCTGCTGCC 19

RESULT 428
AR298254 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR298254
DEFINITION Sequence 9989 from patent US 6537751.
ACCESSION AR298254
VERSION AR298254.1 GI:3168538
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Bacterial markers for use in constructing a high density
JOURNAL Patent: US 6537751-A 9989 25-MAR-2003;
disequilibrium map of the human genome
FEATURES
source 1.20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1348 ATTTTATTTTCCTT 1363
|||||
1 ATTTTATTTTCCTT 16

Db 1 ATTTTATTTTCCTT 16

RESULT 429
AR315939 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR315939
DEFINITION Sequence 6476 from patent US 6559294.
ACCESSION AR315939
VERSION AR315939.1 GI:31709365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths, R., Hoiseh, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
COMMENT OS Artificial Sequence
PN JP 2002528391-A/47
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN, ALAN ROBERT MACLEOD, WILLIAM M SIDERS PC
A61K48/00, A61K31/165, A61K31/19, A61K31/513, A61K31/517, A61K31/PC
706,

Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 TTGCTGTGCTGCTGCC 740
|||||
2 TTGCTGTGCTGCTGCC 17

Db

RESULT 430

AR491020

LOCUS AR491020 20 bp DNA linear PAT 15-MAY-2004

DEFINITION Sequence 114 from patent US 6713300.

ACCESSION AR491020

VERSION AR491020.1 GI:47258553

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 20)
Allikmets, R., Anderson, K.L., Dean, M., Leppert, M., Lewis, R.A.,
Li, Y., Lupski, J.R., Nathans, J., Ratner, A., Shroyer, N.F., Singh, N.,
Smalwood, P. and Sun, H.

Nucleic acid and amino acid sequences for ATP-binding cassette
transporter and methods of screening for agents that modify
ATP-binding cassette transporter

Patent: US 6713300-A 114 30-MAR-2004;

Location/Qualifiers

1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1191 TTGCTGTGCTGCTTT 1206
|||||
5 TTGCTGTGCTGCTTT 20

Db

RESULT 431

AX048436/C

LOCUS AX048436 20 bp DNA linear PAT 12-JAN-2001

DEFINITION Sequence 35 from Patent WO0071747.

ACCESSION AX048436

VERSION AX048436.1 GI:12225600

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

1 Boekenkamp, D., Hoppe, H.U. and Burgstaller, P.
Detection system for separating constituents of a sample and
production and use of the same

Patent: WO 0071747-A 35 30-NOV-2000;

Location/Qualifiers

1..20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Beschreibung der kuenstlichen

Sequenz:Erkennungssystem"

Query Match

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1516 AATTAAAAA 1531
|||||
17 ACTTAAAAA 2

Db

RESULT 432
AX053082 20 bp DNA linear PAT 12-JAN-2001

LOCUS AX053082

DEFINITION Sequence 6 from Patent WO0071703.

ACCESSION AX053082

VERSION AX053082.1 GI:12227139

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Macleod, A.R., Li, Z. and Besterman, J.M.
Inhibition of histone deacetylase

Patent: WO 0071703-A 6 30-NOV-2000;

Methylgene, Inc. (CA)

Location/Qualifiers

1..20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="synthetic oligonucleotide"

Query Match

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCTGTGCTGCTGCC 741
|||||
4 TGCTGTGCTGCTGCC 19

Db

RESULT 433

AX053091

LOCUS AX053091 20 bp DNA linear PAT 12-JAN-2001

DEFINITION Sequence 15 from Patent WO0071703.

ACCESSION AX053091

VERSION AX053091.1 GI:12227148

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

1 Macleod, A.R., Li, Z. and Besterman, J.M.
Inhibition of histone deacetylase

Patent: WO 0071703-A 15 30-NOV-2000;

Methylgene, Inc. (CA)

Location/Qualifiers

1..20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Description of Combined DNA/RNA Molecule: Positions

1-4 and 17-20 are 2'-methoxyribose substituted

nucleotides; positions 5-16 are deoxyribonucleotides"

Query Match

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCTGTGCTGCTGCC 741
|||||
4 TGCTGTGCTGCTGCC 19

Db

RESULT 434

AX184293/C

LOCUS AX184293 20 bp DNA linear PAT 06-AUG-2001

DEFINITION Sequence 2046 from Patent WO0142511.

ACCESSION AX184293

VERSION AX184293.1 GI:15135639

KEYWORDS

SOURCE

ORGANISM

1 Homo sapiens (human)

```
REFERENCE
AUTHORS      1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE        Daly M., Hudson T.J., Lander E.S., Rioux J. and Simionovitch K.
JOURNAL      Jb-d-related polymorphisms
              Patent: WO 0142511-A 2546 14-JUN-2001;
              WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipse
              Biotherapeutics Corporation (CA)
FEATURES
source       1..20
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1311 TTATTTTTCAGACAG 1327
Db      20 TTATTTTNGACAG 4

RESULT 435
AX546302
LOCUS      AX546302 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 51 from Patent EP1243290.
ACCESSION  AX546302
VERSION     AX546302.1 GI:25811493
KEYWORDS
SOURCE
ORGANISM    . synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1 Besterman J.M., Macleod A.R. and Siders W.M.
TITLE        Modulation of gene expression by combination therapy
JOURNAL      Patent: EP 1243290-A 51 25-SEP-2002;
              MethyIgene, Inc. (CA)
FEATURES
source       1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"

Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      726 TGCTGTTGCTGCTGCC 741
Db      4 TGCTGCTGCTGCTGCC 19

RESULT 436
AX546392
LOCUS      AX546392 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 51 from Patent EP1243289.
ACCESSION  AX546392
VERSION     AX546392.1 GI:25811583
KEYWORDS
SOURCE
ORGANISM    . synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1 Besterman J.M., Macleod A.R. and Siders W.M.
TITLE        Modulation of gene expression by combination therapy
JOURNAL      Patent: EP 1243289-A 51 25-SEP-2002;
              MethyIgene, Inc. (CA)
FEATURES
source       1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1298 TTAATCTATTTTATT 1316
Db      19 TTGATTTCTTTTATT 1

RESULT 438
A90381/c
LOCUS      A90381 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 562 from Patent EP0856579.
ACCESSION  A90381
VERSION     A90381.1 GI:6738895
KEYWORDS
SOURCE
ORGANISM    . unidentified
              unidentified
              unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 19)
              Brysch W.D. and Schlingensiepen K.D.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: EP 0856579-A 562 05-AUG-1998;
              BIOGNOSTIK GES (DE)
FEATURES
source       1..19
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1298 TTAATCTATTTTATT 1316
Db      19 TTGATTTCTTTTATT 1

RESULT 439
A88414/c
LOCUS      A88414 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 562 from Patent WO9833904.
ACCESSION  A88414
VERSION     A88414.1 GI:6736984
KEYWORDS
SOURCE
ORGANISM    . unidentified
              unidentified
              unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 19)
              Brysch W. and Schlingensiepen K.
TITLE        AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL      Patent: WO 9833904-A 562 06-AUG-1998;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source       1..19
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1298 TTAATCTATTTTATT 1316
Db      19 TTGATTTCTTTTATT 1

RESULT 437
A88414/c
LOCUS      A88414 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 562 from Patent WO9833904.
ACCESSION  A88414
VERSION     A88414.1 GI:6736984
KEYWORDS
SOURCE
ORGANISM    . unidentified
              unidentified
              unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 19)
              Brysch W. and Schlingensiepen K.
TITLE        AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL      Patent: WO 9833904-A 562 06-AUG-1998;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source       1..19
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      726 TGCTGTTGCTGCTGCC 741
Db      4 TGCTGCTGCTGCTGCC 19

Query Match      1.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1298 TTAATCTATTTTATT 1316
Db      19 TTGATTTCTTTTATT 1

RESULT 437
A88414/c
LOCUS      A88414 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 562 from Patent WO9833904.
ACCESSION  A88414
VERSION     A88414.1 GI:6736984
KEYWORDS
SOURCE
ORGANISM    . unidentified
              unidentified
              unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 19)
              Brysch W. and Schlingensiepen K.
TITLE        AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL      Patent: WO 9833904-A 562 06-AUG-1998;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source       1..19
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1311 TTATTTTTCAGACAG 1327
Db      20 TTATTTTNGACAG 4
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BD184608/c
LOCUS BD184608 19 bp DNA linear PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papilloma viruses.
ACCESSION BD184608.1 GI:31876808
VERSION JP 2002360271-A/587.
KEYWORDS Synthetic construct
SOURCE Synthetic construct
ORGANISM Artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ling, C., Lin, R., Yoo, Z., Huang, X., Lee, B., Lee, S., Lin, Y., Huang, C., Hsu, H., Shi, C., Yeh, C., Cao, Y., and Pan, C.
TITLE Method and detector for identifying subtypes of human papilloma
JOURNAL Patent: JP 2002360271-A 587 17-DEC-2002;
KING CAR FOOD INDUSTRIAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360271-A/587
PD 17-DEC-2002
PF 28-NOV-2001 JP 2001362595
PR 04-MAY-2001 TW 90110785
PI CHING-YEH LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSUAN HUANG, BOW-PI HAENG LEE,
PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-PI WEN SHI,
PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN
PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC
, C12Q1/70, G01N21/64,
PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1.93),
CC Oligonucleotide M806108 for identifying HPV CP8061. FH Key
Location/Qualifiers
FT source 1..19 /organism='Artificial Sequence'.
FEATURES
source 1..19 Location/Qualifiers
1..19 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 847 GCCCTTAGTATGATGCA 865
DB 19 GTCCTCCAGTATGATGCA 1
RESULT 440
LOCUS AR294423 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6158 from patent US 6537751.
ACCESSION AR294423
VERSION AR294423.1 GI:31681707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen, D., Chumakov, I., and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL diallelic map of the human genome
FEATURES Patent: US 6537751-A 6158 25-MAR-2003;
Location/Qualifiers
1..19
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1105 TAACCTCCATTTTCCCC 1123
DB 1 TACTTTCTATTTTCCCC 19
RESULT 441
LOCUS AX132831 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 4049 from Patent WO0130362.
ACCESSION AX132831
VERSION AX132831.1 GI:14139141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 4049 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
FEATURES
source 1..19 /organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
/note='PCNA HH ribozyme binding site'
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1299 TAATCTATTTTATTTT 1317
DB 1 TAACCTATTTTCTCT 19
RESULT 442
LOCUS AX352893 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 99 from Patent EP1174518.
ACCESSION AX352893
VERSION AX352893.1 GI:18617975
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Loukachov, V.V., van Gemen, B., and Goudsmilt, J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 99 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
Location/Qualifiers
FEATURES
source 1..19 /organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='position 65'
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1303 CTATTTTCTATTTTCAG 1321
DB 19 CTATTTTCTTCTATAG 1
RESULT 443
LOCUS AX362738 19 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 99 from Patent WO0208463.

ACCESSION AX362738
VERSION AX362738.1 GI:18694878
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Loukachov,V.V., Goudsmit,V. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 99 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 65"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1303 CTATTTTATTTCAG 1321
DB 19 CTATTTTCTTTATAG 1

RESULT 444
AX742755/c 19 bp DNA linear PAT 12-MAY-2003
LOCUS AX742755
DEFINITION Sequence 558 from Patent EP1302550.
ACCESSION AX742755
VERSION AX742755.1 GI:30576744
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
Pan,C.L. and Chan,P.
TITLE Method and detector for identifying subtypes of human papilloma
JOURNAL Patent: EP 1302550-A 558 16-APR-2003;
King Car Food Industrial Co., Ltd. (TW)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide for identifying HPV CP8061"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 847 GCCCTTAGTAGTACGA 865
DB 19 GTCTCCAGTATGTACGA 1

RESULT 445
BD065927/c 19 bp DNA linear PAT 27-AUG-2002
LOCUS BD065927
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065927
VERSION BD065927.1 GI:22611530
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Schlingensiefen,K.H. and Brysch,W.

TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 562 07-AUG-2001;
BIOGENOSITIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/562
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FEATURES
FT source 1..19
Location/Qualifier
FT
source
1..19
/organism="Unknown"
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1298 TTATCTATTTTATT 1316
DB 19 TTGATTTCTTTTATT 1

RESULT 446
A40129 20 bp DNA linear PAT 05-MAR-1997
LOCUS A40129
DEFINITION Sequence 5 from Patent WO9423026.
ACCESSION A40129
VERSION A40129.1 GI:2296287
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Vaessur,M., Blumenfeld,M., Meguenni,S. and Poddevin,B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
JOURNAL Patent: WO 9423026-A 5 13-OCT-1994;
GENSET (FR)
COMMENT Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAAG 1538
DB 1 AAAAAAAAAAATGAAG 19

RESULT 447
A70736 20 bp DNA linear PAT 07-MAY-1999
LOCUS A70736
DEFINITION Sequence 57 from Patent WO9813490.
ACCESSION A70736
VERSION A70736.1 GI:4774739
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)

AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE A gene related to migraine in man
JOURNAL Patent: WO 9813490-A 57 02-APR-1998;
ORHOF ROEL ANDRE (NL)
FEATURES Location/Qualifiers
source 1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1634 TCCTACCCCTTTGAAT 1652
Db 1 TCCTTCCTTCCTTTGTAGAT 19

RESULT 448
LOCUS A79220 20 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 57 from Patent EP0834561.
ACCESSION A79220
VERSION A79220.1 GI:6092265
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS A GENE RELATED TO MIGRAINE IN MAN
TITLE Patent: EP 0834561-A 57 08-APR-1998;
JOURNAL UNIV LEIDEN (NL)
FEATURES Location/Qualifiers
source 1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1634 TCCTACCCCTTTGAAT 1652
Db 1 TCCTTCCTTCCTTTGTAGAT 19

RESULT 449
LOCUS AR086304 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 125 from patent US 5985558.
ACCESSION AR086304
VERSION AR086304.1 GI:10013070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
inhibition of c-Jun and c-Fos
JOURNAL Patent: US 5985558-A 125 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1290 TTGTGCTTAATCTATT 1308
Db 19 TTGTGCTTTAATTATT 1

RESULT 450
LOCUS AR086311 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 132 from patent US 5985558.
ACCESSION AR086311
VERSION AR086311.1 GI:10013077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
inhibition of c-Jun and c-Fos
JOURNAL Patent: US 5985558-A 132 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1290 TTGTGCTTAATCTATT 1308
Db 19 TTGTGCTTTAATTATT 1

RESULT 451
LOCUS AR129739 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 143 from patent US 6187545.
ACCESSION AR129739
VERSION AR129739.1 GI:14117636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Butler,M.M., Wyatt,J. and Cowseert,L.M.
TITLE Antisense modulation of peptk-cyclosolic expression
JOURNAL Patent: US 6187545-A 143 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1563 GCCAGCCCAACAGTGTAT 1581
Db 2 GCCAGCCCAACAGTGTAT 20

RESULT 452
LOCUS AR142677 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6203988.
ACCESSION AR142677
VERSION AR142677.1 GI:15103963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

AUTHORS Kambara,H. and Uematsu,C.
TITLE DNA fragment preparation method for gene expression profiling
JOURNAL Patent: US 6203988-A 7 20-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1306 TTTTATTATTTCAGACA 1324
Db 19 TTTTATTATTTCAGACA 1

RESULT 453
ARI58717 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 339 from patent US 6251588.
DEFINITION ARI58717
ACCESSION ARI58717
VERSION ARI58717.1 GI:16220917
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 339 26-JUN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1246 TCTTGTGTTGTTTAA 1264
Db 2 TCTGTGATTTGTTTAA 20

RESULT 454
ARI58718 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 340 from patent US 6251588.
DEFINITION ARI58718
ACCESSION ARI58718
VERSION ARI58718.1 GI:16220919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 340 26-JUN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1246 TCTTGTGTTGTTTAA 1264
Db 1 TCTGTGATTTGTTTAA 19

RESULT 455
ARI63731 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 18 from patent US 6271029.
DEFINITION ARI63731
ACCESSION ARI63731
VERSION ARI63731.1 GI:16234426
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, and Cowseert,L.M.
TITLE Antisense inhibition of cyclohesin-2 expression
JOURNAL Patent: US 6271029-A 18 07-AUG-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 352 GCCCGCAGAGGGGCTCG 370
Db 1 GTCCCGCAGTCGGGCTCG 19

RESULT 456
ARI69510 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 6 from patent US 6291173.
DEFINITION ARI69510
ACCESSION ARI69510
VERSION ARI69510.1 GI:17907377
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bartel,P.L. and Tavtigian,S.V.
TITLE WMS2--an MMAC1 interacting protein
JOURNAL Patent: US 6291173-A 6 18-SEP-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1238 CTTCTCATCTTTGTTTG 1256
Db 1 CTTCTCTCTTTGTATAG 19

RESULT 457
ARI76870 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 125 from patent US 6312900.
DEFINITION ARI76870
ACCESSION ARI76870
VERSION ARI76870.1 GI:17919225
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the modulation of activating protein 1
JOURNAL Patent: US 6312900-A 125 06-NOV-2001;

FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGCTAATCTATT 1308
|||||
19 TTGTGTATTATTTATT 1

Db 19 TTGTGTATTATTTATT 1

RESULT 458
AR176877/c AR176877 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 132 from patent US 6312900.
DEFINITION AR176877
ACCESSION AR176877
VERSION AR176877.1 GI:17919232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
modulation of activating protein 1
JOURNAL Patent: US 6312900-A 132 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGCTAATCTATT 1308
|||||
19 TTGTGTATTATTTATT 1

Db 19 TTGTGTATTATTTATT 1

RESULT 459
E05497 E05497 20 bp DNA linear PAT 29-SEP-1997
LOCUS PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
DEFINITION E05497
ACCESSION E05497
VERSION E05497.1 GI:2173685
KEYWORDS JP 1993244995-A/7.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Komatsu,Y. and Kikuchi,Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
KYOMA HAKKO KOGYO CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
OS Zea maize
PN JP 1993244995-A/7
PD 24-SEP-1993
PF 24-SEP-1991 JP 1991244122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C1201/68,C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES Location/Qualifiers
source 1..20

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 545 TTGTGTGCTGTCGTCGTC 563
|||||
1 TGTGTGTGTGTGTGTGC 19

Db 1 TGTGTGTGTGTGTGTGC 19

RESULT 460
E28096/c E28096 20 bp DNA linear PAT 18-JUN-2001
LOCUS Method for analyzing DNA fragment.
DEFINITION E28096
ACCESSION E28096
VERSION E28096.1 GI:13018321
KEYWORDS JP 1999196874-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Hideki,K. and Senshu,U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 7 27-JUL-1999;
HITACHI LTD
OS Unidentified
PN JP 1999196874-A/7
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR HIDEKI KAMIBARA,SENSHU UEMATSU
PI C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
PC C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..20
Location/Qualifiers
FT source 1..20
/organism="Unidentified".
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1306 TTTTGTATTTCAGACA 1324
|||||
19 TTTTGTATTTCAGACA 1

Db 19 TTTTGTATTTCAGACA 1

RESULT 461
E44159/c E44159 20 bp DNA linear PAT 27-AUG-2002
LOCUS Methods of identification and specific detection of slow-growing
DEFINITION E44159 mycobacteria by using characteristic base sequence occurring in DNA
gyrase gene.
ACCESSION E44159
VERSION E44159.1 GI:22553300
KEYWORDS JP 2001128679-A/2.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Kasai,H., Ezaki,T. and Harayama,S.
TITLE Methods of identification and specific detection of slow-growing
mycobacteria by using characteristic base sequence occurring in DNA
gyrase gene
JOURNAL Patent: JP 2001128679-A 2 15-MAY-2001;

COMMENT MARINE BIOTECHNOLOGY INST CO LTD
OS Artificial Sequence
PN JP 2001128679-A/2
PD 15-MAY-2001
PF 02-NOV-1999 JP 1999312525
TITLE HIROAKI KASAI, TAKAYUKI EZAKI, SHIGEAKI HARAYAMA PC
C12N15/09, C12Q1/04, C12Q1/68, C12N15/00
CC

FEATURES
source Location/Qualifiers.
FH Key 1.20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 348 GCAGCGCGCGCGAGGCGC 366
DB 19 CGCGCGCGCGCGCAAGGTC 1

RESULT 462
LOCUS E59328 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS JP 2000342265-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose K. and Yoshida, T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TOGOSEI CHEM IND CO LTD
OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR KUNIHICO HIROSE, TADAO YOSHIDA
PI C12N15/09, B01D15/08, C12N15/00
PC
CC

FEATURES
source Location/Qualifiers.
FH Key 1.20
/organism="Artificial Sequence".
FT source 1.20
Location/Qualifiers
1.20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1519 TAAAAAAGAAAGTAAAA 1537
DB 1 TAAAAAAGAAAGTAAAA 19

RESULT 463
LOCUS I17092 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 7 from patent US 5484703.
ACCESSION I17092
VERSION I17092.1 GI:1252000
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown:
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Raben, N.; Nichols, R., Plotz, P. and Leff, R.
TITLE Assay using recombinant histidyl-tRNA synthetase
JOURNAL Patent: US 5484703-A 7 15-JAN-1996;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1032 GCAGAGTGGCGGCGGTGG 1050
DB 1 GCAGAGCGTGGCGGCGCTGG 19

RESULT 464
LOCUS I63487 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5663066.
ACCESSION I63487
VERSION I63487.1 GI:2481060
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Raben, N.; Nichols, R., Plotz, P. and Leff, R.
TITLE Assay using recombinant histidyl-tRNA synthetase
JOURNAL Patent: US 5663066-A 7 02-SEP-1997;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1032 GCAGAGTGGCGGCGGTGG 1050
DB 1 GCAGAGCGTGGCGGCGCTGG 19

RESULT 465
LOCUS AR200176/c 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 51 from patent US 6355782.
ACCESSION AR200176
VERSION AR200176.1 GI:20250250
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zonana, J., Ferguson, B.M., Headon, D. and Overbeek, P.
TITLE Hypohidrotic ectodermal dysplasia genes and proteins
JOURNAL Patent: US 6355782-A 51 12-MAR-2002;
FEATURES Location/Qualifiers
source 1.20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1018 ACCTGAGATTGACGCAGA 1036
DB 11 | | | | | | | | | | | | | | | | | | | | | |

Db 19 ACATGAGAAATGACGCTGA 1

RESULT 466

LOCUS AR224778 20 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 83 from patent US 6440739.

ACCESSION AR224778

VERSION AR224778.1 GI:23333618

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Bennett,C.F. and Freier,S.M.

TITLE Antisense modulation of glioma-associated oncogene-2 expression

JOURNAL Patent: US 6440739-A 83 27-AUG-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1627 CAATCTCTCCCTACCTTT 1645

Db 2 CAATGCTCCCTACCTCT 20

RESULT 467

LOCUS AR307902 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 113 from patent US 6551826.

ACCESSION AR307902

VERSION AR307902.1 GI:31698658

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Walt,A.T.

TITLE Antisense modulation of raiid expression

JOURNAL Patent: US 6551826-A 113 22-APR-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1540 GAAGGACGAGATGCACCA 1558

Db 1 GAAGGACGAGATGCACCA 19

RESULT 468

LOCUS AR313596/c 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 4133 from patent US 6559294.

ACCESSION AR313596

VERSION AR313596.1 GI:31707022

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Griffiths,R., Holseih,S.K., Zagureky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 4133 06-MAY-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 985 GGACGTTCTGTTCTGTGG 1003

Db 20 GGACCTACTTTTCTGTGG 2

RESULT 469

LOCUS AR314906/c 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 5443 from patent US 6559294.

ACCESSION AR314906

VERSION AR314906.1 GI:31708332

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Griffiths,R., Holseih,S.K., Zagureky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 5443 06-MAY-2003;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 706 TGGAGTGGCGTTCCTCTT 724

Db 20 TGGAGTGGCGTTCCTCTT 2

RESULT 470

LOCUS AR371268 20 bp DNA linear PAT 12-SEP-2003

DEFINITION Sequence 4 from patent US 6395474.

ACCESSION AR371268

VERSION AR371268.1 GI:34608200

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.

TITLE Peptide nucleic acids

JOURNAL Patent: US 6395474-A 4 28-MAY-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAAG 1538

Db 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 471

AR428075/c
LOCUS AR428075 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6641818.
ACCESSION AR428075
VERSION AR428075.1 GI:40187443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Spear,P.G., Warner,M.S., Geraghty,R.J., Martinez,W.M.,
Montgomery,R.I., Cohen,G.H., Eisenberg,R.V., Whitebeck,C.J. and
Krummenacher,C.
TITLE Cellular proteins which mediate herpesvirus entry
JOURNAL Patent: US 6641818-A 5 04-NOV-2003;
FEATURES
LOCATION/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 TGCTGTTGCTGCTGCTTT 744
DB 19 TGCTGTTGCTGCTGCTTT 1

RESULT 472
AR489489 20 bp DNA linear PAT 15-MAY-2004
LOCUS AR489489
DEFINITION Sequence 4 from patent US 6710163.
ACCESSION AR489489
VERSION AR489489.1 GI:47256514
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid EYTHONs
JOURNAL Patent: US 6710163-A 4 23-MAR-2004;
FEATURES
LOCATION/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAG 1538
DB 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 473
AR491100 20 bp DNA linear PAT 15-MAY-2004
LOCUS AR491100
DEFINITION Sequence 4 from patent US 6713602.
ACCESSION AR491100
VERSION AR491100.1 GI:47258960
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 4 30-MAR-2004;
FEATURES
LOCATION/Qualifiers
1..20

/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAG 1538
DB 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 474
AX078001 20 bp DNA linear PAT 22-FEB-2001
LOCUS AX078001
DEFINITION Sequence 15 from patent WO0105435.
ACCESSION AX078001
VERSION AX078001.1 GI:13157746
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gleave,M.
TITLE Antisense therapy for hormone-regulated tumors
JOURNAL Patent: WO 0105435-A 15 25-JAN-2001;
FEATURES
LOCATION/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1304 TATTTTATTTTTCAGA 1322
DB 2 TTTTATTTTTCAGAA 20

RESULT 475
AX078001/c 20 bp DNA linear PAT 22-FEB-2001
LOCUS AX078001
DEFINITION Sequence 15 from patent WO0105435.
ACCESSION AX078001
VERSION AX078001.1 GI:13157746
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gleave,M.
TITLE Antisense therapy for hormone-regulated tumors
JOURNAL Patent: WO 0105435-A 15 25-JAN-2001;
FEATURES
LOCATION/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TTAATAAAAAAAAAAGTAA 1536
DB 19 TTGAAAAAAAAAAAAAAAAA 1

RESULT 476
 LOCUS AX137428/c 20 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 3 from Patent EP1098003.
 ACCESSION AX137428
 VERSION AX137428.1 GI:14273633
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 Kasei, H., Harayama, S. and Ezaki, T.
 Identification method and specific detection method of slow growing
 mycobacteria utilizing dna gyrase gene
 Patent: EP 1098003-A 3 09-MAY-2001;
 JOURNAL MARINE BIOTECHNOLOGY INSTITUTE CO., LTD. (JP)
 FEATURES
 source
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 348 CGCCGCCCGCCGACAGCGGC 366
 Db 19 CGCCGCCCGCCGACAGGTC 1

RESULT 477
 LOCUS AX293619/c 20 bp DNA linear PAT 21-NOV-2001
 DEFINITION Sequence 5381 from Patent WO0179548.
 ACCESSION AX293619
 VERSION AX293619.1 GI:17055302
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
 Method of designing addressable array for detection of nucleic acid
 sequence differences using ligase detection reaction
 Patent: WO 0179548-A 5381 25-OCT-2001;
 JOURNAL CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES
 source
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1184 ACGCGATTCTGCTGCTGCT 1202
 Db 19 ACGCGATTCTGCTGCTGCT 1

RESULT 478
 LOCUS AX298452 20 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 86 from Patent WO0183749.
 ACCESSION AX298452
 VERSION AX298452.1 GI:17128442
 KEYWORDS
 SOURCE
 Mus sp.

ORGANISM
 Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,
 Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Torold, M.G.
 Gene and sequence variation associated with sensing carbohydrate
 compounds and other sweeteners
 Patent: WO 0183749-A 86 08-NOV-2001;
 JOURNAL WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
 (US)

FEATURES
 source
 1..20
 /organism="Mus sp."
 /mol_type="unassigned DNA"
 /db_xref="taxon:10095"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1227 CTAGCTTACCTTCTCTCA 1245
 Db 2 CAACTCTTACCTTCTCTCA 20

RESULT 479
 LOCUS AX452909/c 20 bp DNA linear PAT 06-JUL-2002
 DEFINITION Sequence 10 from Patent WO0242322.
 ACCESSION AX452909
 VERSION AX452909.1 GI:21712544
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 Jackson, D., Casari, G. and Suckow, J.
 Mammalian nuclear receptor cofactors c7 and c8 and methods of use
 Patent: WO 0242322-A 10 30-MAY-2002;
 JOURNAL LION Bioscience AG (DE)
 FEATURES
 source
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer for amplifying CF8"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
 Db 20 AATAAGAAAAAGTAAAG 2

RESULT 480
 LOCUS AX462672/c 20 bp DNA linear PAT 15-JUL-2002
 DEFINITION Sequence 416 from Patent EP1217079.
 ACCESSION AX462672
 VERSION AX462672.1 GI:21885885
 KEYWORDS
 SOURCE
 ORGANISM
 Aegilops tauschii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Aegilops.

REFERENCE
 1 Bernard, M., Sourdil, P. and Guyomarch, H.
 Microsatellite markers from Triticum tauschii
 Patent: EP 1217079-A 416 26-JUN-2002;

RESULT 485
BD003450 20 bp DNA linear PAT 31-JAN-2002
LOCUS A gene related to migrate in man.
DEFINITION
ACCESSION BD003450
VERSION BD003450.1 GI:18631411
KEYWORDS JP 2001500743-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Frantz,R.R.I.E., Ferrarri,M.D., Terravinto,H.M. and Ogniofu,R.A.
TITLE 1 (bases 1 to 20)
JOURNAL A gene related to migrate in man
Patent: JP 2001500743-A 19 23-JAN-2001;
RYUKUS UNIVERSITY TO RAIDEN
COMMENT OS Homo sapiens (human)
PN JP 2001500743-A/19
PD 23-JAN-2001
PF 26-SEP-1997 JP 1998515527
PR 27-SEP-1996 EP 96202707.4
PI RENE ROBERT ISAAC,ERIK FRANTZ,MICHEL DOMINIQUE FERRARI, PI
HISRA MARY TERUVINTO,RURU ANDRE OPUHOFU
PC C12N15/09,A01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,
PC C12N1/21
PC C12N5/10,C12N1/02,C12N1/68,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
FT primer bind (1)..(20).
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1634 TCCCTACCCCTTTGAAAT 1652
Db 1 TCCCTTCCCTTTGTAGAT 19

RESULT 486
BD056369 20 bp DNA linear PAT 27-AUG-2002
LOCUS Peptide having a function regulating transcription of gene.
DEFINITION
ACCESSION BD056369
VERSION BD056369.1 GI:22601975
KEYWORDS JP 2001269176-A/3.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Takagi,M., Shinji,H. and Ota,K.
TITLE Peptide having a function regulating transcription of gene
JOURNAL Patent: JP 2001269176-A 3 02-OCT-2001;
AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2001269176-A/3
PD 02-OCT-2001
PF 27-MAR-2000 JP 2000087536
PI MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
PC C12N15/09,C07K14/415,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
C12P21/02.
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),C12N15/00,C12N5/00,
PC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic primer DNA FH
Key Location/Qualifiers
1..20
Location/Qualifiers

FEATURES
source 1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1399 ATGAGTGTCAAGATPAGG 1417
Db 2 ATGCTGTCAAAATPAGG 20

RESULT 487
BD056371 20 bp DNA linear PAT 27-AUG-2002
LOCUS Peptide having a function regulating transcription of gene.
DEFINITION
ACCESSION BD056371
VERSION BD056371.1 GI:22601977
KEYWORDS JP 2001269176-A/5.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Takagi,M., Shinji,H. and Ota,K.
TITLE Peptide having a function regulating transcription of gene
JOURNAL Patent: JP 2001269176-A 5 02-OCT-2001;
AGENCY OF IND SCIENCE & TECHNOL
COMMENT OS Artificial Sequence
PN JP 2001269176-A/5
PD 02-OCT-2001
PF 27-MAR-2000 JP 2000087536
PI MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
PC C12N15/09,C07K14/415,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
C12P21/02.
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),C12N15/00,C12N5/00,
PC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic primer DNA FH
Key Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1399 ATGAGTGTCAAGATPAGG 1417
Db 2 ATGCTGTCAAAATPAGG 20

RESULT 488
BD089539 20 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION
ACCESSION BD089539
VERSION BD089539.1 GI:22635149
KEYWORDS JP 2001321190-A/1783.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1783 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT OS Artificial Sequence
PN JP 2001321190-A/1783
PD 20-NOV-2001

```

PF 12-MAR-2001 JP 2001068285
PI EITCHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N3/53,G01N3/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1549 ATGTCACCCAGATGCCAG 1567
DB 19 ATGCCACTCAGATCCAG 1

RESULT 489
LOCUS BD161924 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized
substrate.
ACCESSION BD161924 GI:27867682
VERSION BD161924.1
KEYWORDS JP 2002191369-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
Tanga,N., Okamura,H. and Takahashi,K.
AUTHORS Method for carrying out thermal cycle of PCR using DNA-immobilized
TITLE substrate
JOURNAL Patent: JP 2002191369-A 1 09-JUL-2002;
TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT OS JP 2002191369-A/1
PN JP 2002191369-A/1
PD 09-JUL-2002
PP 27-DEC-2000 JP 2000399573
PI MICHIYUKI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
Immobilized
CC substrate
FH key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1300 AATCTATTTTATTTT 1318
DB 2 AATTTTTTTTTTTTTTTT 20

RESULT 490
LOCUS S4717684 20 bp DNA linear PRI 08-MAY-1993
DEFINITION lipoprotein lipase (introns 3, 6 and 8) [human, Genomic, 20 nt,
segment 4 of 5].

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ACCESSION S47179 GI:258898
VERSION S47179.1
KEYWORDS 4 of 5
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Goto,T., Yamada,N., Murase,T., Shimano,H., Shinada,M., Harada,K.,
1 (bases 1 to 20)
Gojoda,T., Yamada,N., Murase,T., Shimano,H., Shinada,M., Harada,K.,
Kawamura,M., Kozaki,K. and Yazaki,Y.
TITLE Detection of three separate DNA polymorphisms in the human
lipoprotein lipase gene by gene amplification and restriction
endonuclease digestion
JOURNAL J. Lipid Res. 33 (7), 1067-1072 (1992)
MEDLINE 93057100
PUBMED 1358995
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbon 117241] from the original journal article.
Regions surrounding three polymorphic sites.
COMMENT Location/Qualifiers
source
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1502 AGAAGATCTGTTATTA 1520
DB 20 AGAAGATCTGTTATTA 2

RESULT 491
LOCUS AB068086 20 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-H96854 at
1p36.
ACCESSION AB068086
VERSION AB068086
KEYWORDS AB068086.1 GI:15128890
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takeoka,E., Maekawa,K.,
Matanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Onira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1..20
/note="forward primer for human STS sts-H96854 at 1p36
sts-H96854 obtained from clones B293A18, B122E3, B91D18,
Human BAC library RPCI-11"

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